

GenCore version 5.1.4 p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 27, 2003, 03:58:17 ; Search time 11025 Seconds
(without alignments)
17546.947 Million cell updates/sec

Title: US-09-922-549B-67
Perfect score: 11945
Sequence: 1 tgcgcctctcttgatattc.....tgcgccttgctgctcttaggg 11945

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlin:*
5: em_estcov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	630.4	5.3	699	9	AL584990 AL584990
2	262.6	2.2	673	9	AJ453074 AJ453074
3	238.6	2.0	634	13	BI064896 BI064896
4	222.2	1.9	446	9	AL587961 AL587961
5	220.8	1.8	582	12	BG625446 BG625446
6	210.6	1.8	650	9	AJ453847 AJ453847

7	208.6	1.7	689	9	AJ392780 AJ392780
8	201	1.7	489	10	AM240181 AM240181
9	197.4	1.7	700	9	AJ445833 AJ445833
10	197.4	1.7	826	9	AJ456416 AJ456416
11	193.2	1.6	914	17	GG246112 GG246112
12	191	1.6	437	12	BG624980 BG624980
13	186.4	1.6	608	17	GG0000392 GG0000392
14	183.2	1.5	604	14	B0037358 B0037358
15	183	1.5	581	13	BI388759 BI388759
16	178.8	1.5	582	9	AL588808 AL588808
17	175	1.5	624	13	BM426214 BM426214
18	164.6	1.4	644	9	AL585302 AL585302
19	164.2	1.4	681	9	AJ393361 AJ393361
20	160	1.3	564	13	BI066024 BI066024
21	158.4	1.3	526	13	BM490080 BM490080
22	155	1.3	602	9	AJ455303 AJ455303
23	154.8	1.3	644	13	BI392307 BI392307
24	154.4	1.3	741	9	AL584343 AL584343
25	154.2	1.3	643	13	BM440491 BM440491
26	152.4	1.3	637	13	BM440335 BM440335
27	151.4	1.3	900	14	B0720191 B0720191
28	149	1.2	644	13	BI390882 BI390882
29	148.4	1.2	647	13	BM440702 BM440702
30	148.2	1.2	796	9	AJ444515 AJ444515
31	146.4	1.2	604	17	GG4140117 GG4140117
32	144.4	1.2	634	13	BM486806 BM486806
33	144.2	1.2	562	13	BM426795 BM426795
34	143.4	1.2	483	13	BM489773 BM489773
35	143	1.2	645	13	BM488238 BM488238
36	142.8	1.2	455	17	BM405358 BM405358
37	140.4	1.2	664	13	BI393232 BI393232
38	139.6	1.2	754	9	AJ454778 AJ454778
39	139	1.2	620	14	B0038729 B0038729
40	138.8	1.2	600	17	GG0000010 GG0000010
41	138.4	1.2	804	9	AJ445375 AJ445375
42	137.2	1.1	638	13	BM440658 BM440658
43	135.6	1.1	676	13	BM426719 BM426719
44	134.6	1.1	644	9	AJ981722 AJ981722
45	134.6	1.1	676	10	AM983878 AM983878

ALIGNMENTS

RESULT 1	AL584990	699 bp	mRNA	linear	EST 28-FEB-2001
LOCUS	AL584990	Stratagene Chick Embryo Lambda cDNA Library			
DEFINITION	AL584990	Gallus gallus cDNA clone ROS017A10, mRNA sequence.			
ACCESSION	AL584990				
VERSION	AL584990.1	GI:1163723			
KEYWORDS	EST.				
SOURCE	chicken.				
ORGANISM	Gallus gallus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;				
AUTHORS	Phasianidae; Gallus.				
TITLE	1 (bases 1 to 699)				
JOURNAL	Murray, F.				
COMMENT	Stratagene Chick Embryo Lambda cDNA Library				
	Unpublished (2001)				
	Contact: Frazer Murray				
	Dept. Genomics and Bioinformatics				
	Roslin Institute				
	Roslin, Midlothian, EH25 9PS, UK				
	Tel: +44 (0)131 527 4200				
	Fax: +44 (0)131 440 0434				
	Email: frazer.murray@bbsrc.ac.uk				
	Seq primer: 73.				
FEATURES	location/Qualifiers				
source	1..699				
	/organism="Gallus gallus"				
	/db_xref="taxon:9031"				

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/clone="KOS017A10"
/clone_lib="Stratagene Chick Embryo Lambda cDNA Library (*
937405)"
/issue_type="Embryo"
/dev_stage="5 days old"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Vector: pBLUESCRIPT SK; Site: EcoRI; Site 2: XhoI
/Cloned unidirectionally. Primer: Oligo dt. Uni-ZAP XR
vector. Average insert size: 1.5kb.; 5' adaptor sequence:
5' GAATTCGCGACGAG 3'; 3' adaptor sequence: 5'
CTCGAGTTTCTTTTCTTTT 3'."

BASE COUNT      160 a      127 c      142 g      270 t
ORIGIN

Query Match
Best Local Similarity 98.5%; Pred. No. 2.2e-97;
Matches 678; Conservative 0; Mismatches 6; Indels 4; Gaps 4;

QY 338 GACGACCTTTGGAACTGTACAGCCCTTTCTTCATTCCTTTTTCCTGTCGCC 397
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 14 GCAGAGCTTTTGGAACTGTACAGCCCTTTCTTCATTCCTTTTTCCTGTCGCC 73

QY 398 AATGCTTTGGTTGATTTGATTTGAAACGTTGATCGAAGCTTGAAGTTTATTT 457
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 74 AATGCTTTGGTTGATTTGATTTGAAACGTTGATCGAAGCTTGAAGTTTATTT 133

QY 458 ATAGTGTGCTTGAAGCTTGAAGTGTGTTTACACAGATACCTTATTAAGTTAGG 517
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 134 ATAGTGTGCTTGAAGCTTGAAGTGTGTTTACACAGATACCTTATTAAGTTAGG 193

QY 518 CCAGCTTGATCTTATTTTCCCTTTGAAGTGTAGGCTTCTGCTTTTTCCTT 577
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 194 CCAGCTTGATCTTATTTTCCCTTTGAAGTGTAGGCTTCTGCTTTTTCCTT 253

QY 578 TGAAGCTGTGAGGCTTATTTTCTAATGAGATTTTTCACGATATCATGTTGAT 637
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 254 TGAAGCTGTGAGGCTTATTTTCTAATGAGATTTTTCACGATATCATGTTGAT 313

QY 638 ACCCAATGCTTGAATGTTTCTTACTAATGATGATGATTCGATTTACATGTT 697
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 314 ACCCAATGCTTGAATGTTTCTTACTAATGATGATGATTCGATTTACATGTT 373

QY 698 GTATATCTTGTCACTGCTGTTTCTAGTAAATATATGATTTATGAATATGTAAT 757
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 374 GTATATCTTGTCACTGCTGTTTCTAGTAAATATATGATTTATGAATATGTAAT 432

QY 758 TCTGATTTTCC-TTTTTTTTATCTATGCTGTGTGTACAGTCAACAGACTTAC 816
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 433 TCTGATTTTCC-TTTTTTTTATCTATGCTGTGTGTACAGTCAACAGACTTAC 492

QY 817 TCTATATTTTATATAGATTTTATATGAGTGTGCTGTTGTTCTTGTGTAAGA 876
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 493 TCTATATTTTATATAGATTTTATATGAGTGTGCTGTTGTTCTTGTGTAAGA 551

QY 877 TACAGCCTTAATTTCCAGAGCATGCTCAGTAAAGGGGTTGTACATGGTTCAAT 936
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 552 TACAGCCTTAATTTCCAGAGCATGCTCAGTAAAGGGGTTGTACATGGTTCAAT 611

QY 937 GTAAGAGGAGCGCTTTGGCTGCTGCCGATCCGAGATCCAGACACTAAACGTC-TTCG 995
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 612 GTAAGAGGAGCGCTTTGGCTGCTGCCGATCCGAGATCCAGACACTAAACGTCG 671

QY 996 CACTGAGGTATTAATTCGCTCAGATCCC 1023
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 672 CACTGAGGTATTAATTCGCTCAGATCCC 699

RESULT 2
LOCUS      A4453074      673 bp      mRNA      linear      EST 22-APR-2002
DEFINITION A4453074 riken1 Gallus gallus cDNA clone 33c3r1, mRNA sequence.
ACCESSION A4453074
VERSION    A4453074.1 GI:20263170
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KEYWORDS    EST.
SOURCE      chicken.
ORGANISM    Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1 (bases 1 to 673)
AUTHORS    Buerstedde,J.M.
TITLE      Gallus gallus bursal lymphocyte EST
JOURNAL    unpublished (2002)
COMMENT     Contact: Buerstedde JM
            Cellular Immunology
            Heinrich-Pette-Institute
            Martinistr. 52, 20251 Hamburg, Germany
            Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.

FEATURES
  source
    1..673
    /organism="Gallus gallus"
    /db_xref="taxon:9031"
    /clone="33c3r1"
    /clone_lib="riken1"
    /cell_type="bursal lymphocyte"
    /dev_stage="--2-3 weeks old"
    /note="CB inbred strain"

BASE COUNT      140 a      201 c      156 g      176 t
ORIGIN

Query Match
Best Local Similarity 81.3%; Pred. NO. 8.7e-35;
Matches 378; Conservative 0; Mismatches 54; Indels 33; Gaps 5;

QY 10572 TCATAGATCATAGATGCGCTGGTTGAAGGAGACCCCAAGATCATGAATCCACA 10631
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 223 TTACGATTCATAGATGCGCTGGTTGAAGGAGACCCCAAGATCATGAATCCACA 279

QY 10632 CCCCCGACAGGAGGCGCCACCACTCCAGATGTGTACTAGACCGACGCCAGG 10691
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 280 CCCCCGACAGGAGGCGCCACCACTCCAGATGTGTACTAGACCGACGCCAGG 339

QY 10692 CTCATCCACCTGCGCATGAACACCTCCAGAGATGAGACATCCACACCTCTGGGCA 10751
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 340 CTCATCCACCTGCGCATGAACACCTCCAGAGATGAGACATCCACACCTCTGGGCA 399

QY 10752 GCTGTGCCACACCTCACACCTCTCTGTGAAGACCTTTTCCCTGCATCAATCTAA 10811
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 400 GCTGTGCCACACCTCACACCTCTCTGTGAAGACCTTTTCCCTGCATCAATCTAA 457

QY 10812 GCTTCCCTCTGTGAGTTAATCCATCCCTGCTGTACTGCTACTGCTACTGTTAA 10871
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 458 GCTTCCCTCTGTGAGTTAATCCATCCCTGCTGTACTGCTACTGCTACTGTTAA 517

QY 10872 AAAGTTGATTCCTCCCTTTT-----TGAAAGTTGCAATGAGGTC 10912
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 518 AAAGTTGATTCCTCCCTTTTATAATCTCTTCTTAATACGGAAGGCTGTAATGAGTC 577

QY 10913 TCTTTGAGCCTTCTTCTCTCTGCGAGAGTGAACAAGCCAGCTCCCTGCTCTTT 10972
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 578 TCTTTGAGC-----TTTCTCGAGGCTGACAAAGCCAGCTCCCTGCTCTTTCT 629

QY 10973 ATAGAGAGGTGCTCCAGCCTCTGATCATCTTTTGCCCTCTCT 11017
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 630 ATAGAGAGGTGCTCCA-CCCTGATGCTCTTTTGCCCTCTCT 673

RESULT 3
LOCUS      B1064896      634 bp      mRNA      linear      EST 15-JUN-2001
DEFINITION B1064896 pf1n.pk002.n24 normalized chicken fat cDNA library Gallus gallus
            cDNA clone pf1n.pk002.n24 5' similar to pf1A4718|A4718 reverse
            transcriptase, pol-like - chicken (fragment) gb|AA49027.1| (L22152
            ) reverse transcriptase [gallus gallus]c, mRNA sequence.
ACCESSION    B1064896
VERSION      B1064896.1 GI:14472418
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KEYWORDS	EST
SOURCE	chicken.
ORGANISM	Gallus gallus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. 1 (bases 1 to 634)
AUTHORS	Cogburn,L.A., Morgan,R.W. and Burnside,J.
TITLE	Chicken ESTs from fat
JOURNAL	Unpublished (2001)
COMMENT	Contact: Larry A. Cogburn University of Delaware Townsend Hall, Newark, DE 19717, USA Tel: 302-831-1335 Fax: 302-831-2822 Email: cogburn@udel.edu, www.chickest.udel.edu.
FEATURES	Location/Qualifiers
source	1..634 /organism="Gallus gallus" /db_xref="taxon:9031" /clone_pfln:"PK002.n24" /clone_lib="normalized chicken fat cDNA library" /sex="Male and female" /tissue_type="fat" /lab_host="E.coli EMDH10B" /note="Vector: pSPORI1"
BASE COUNT	139 a 186 c 122 g 178 t 9 others
ORIGIN	
Query Match	2.0%; Score 238.6; DB 13; Length 634;
Best Local Similarity	67.7%; Pred. No. 1,1e-30;
Matches	388; Conservative 0; Mismatches 180; Indels 5; Gaps 4;
OY	10613 GGATCATGAAGATCCACACCCTGGCCAGCAGGCGCCACCAACCTTCAGATCTGTGTAC 10672
Db	1 GGATCATGAAGTGCACGCCCTTGCTGCGAGAAGGTGTCACTGTCAATGCAATCAAGCAC 60
OY	10673 TAGACCAAGCAGCCAGGCGCTCATCAACCGCGCATTAACAACCTCCAGGATGAGCA 10732
Db	61 TGGCGAGGTTGCCATGCTCCATGACCCGTGGCCCTGTAAAGCCTTGGGGATGGGCA 120
OY	10733 TCACACACCTCTCTGTGGGAGCCCTGTGCCAGCACTCA -CCACCCTCTGTGAAGAATT 10791
Db	121 TCACACAGCCTCTGGACCAACCTGTGTCCCAGGGGTCTACACCACCTCTCAGTGGAAAACT 180
OY	10792 TTCCCTGACATCCATCTRAAGCTTCCCTCTTGAGGTTAGTTCACACTCCCCCTGTGCT 10851
Db	181 TTGCTGACATCTAATCTAAATTTTCCCTTGTAGTTTAAACATAATCTCTCTGTCCG 240
OY	10852 ATCACTGTCT -ACTCTTGAANAAGTGTATCTCCCTTTTGGAGGTTCATATGAGG 10910
Db	241 ATTGCTGTCTGTTTAAAAAAAAAAAAAACTTCTCTTCTGTATTAATTCCTCTTAAAG 300
OY	10911 TCTCTTCAGAGCCTCTTCTCTTTCGACAGATGAACAAGCCAGCTCCCTACGCTGTCT 10970
Db	301 TATTGTAGGCAATTAACAAGTCTCCCCACATCAACAAGCCAGCTTCTCAGCGTCT 360
OY	10971 TTATAGAGAGGTGCTCCAGCCCTGTGATCATCTTTGTGGCCCTCTCTGGACCGCTCC 11030
Db	361 TCAATGTAGAGATGTCTCCACCTCTTCATCATCTTTGTGGCCCTCTC -AGACCTCTTCC 419
OY	11031 AAGACCTCCACATCTTCTCTGTACGTGGGGGCCCGCAGGCTGTAATGCAGATCTCCAGATG 11090
Db	420 AAAACCTAGTATCTT --CTGTGTAGTGTGGCCCGCAGACTGGATGTCAGTACCAATG 477
OY	11091 GCCCTCAAAGAGCAGAGTAAAAGAGGAGCAATCACTTCTCACTCTGCTGGCCAGCCT 11150
Db	478 GCCCTCATATATGTGTAGAGAGAGAGGAGATGCTCACTCTCCATCAGCTGAGCCACTCT 537
OY	11151 CTTTGATGAGGCTCGATTAACAATCTGGCTTC 11183
Db	538 TTTTGTATGTNNCCNNTACTGTGTCTCCG 570

AL587961	AL587961	446 bp	mRNA	linear	EST 02-MAR-2001
LOCUS	AL587961 BP Chicken Brain Library Gallus gallus cDNA clone				
DEFINITION	ROS065F10 mRNA sequence.				
ACCESSION	AL587961				
VERSION	AL587961.1 GI:13192995				
KEYWORDS	EST.				
SOURCE	chicken.				
ORGANISM	Gallus gallus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;				
AUTHORS	Archosauirita; Aves; Neognathae; Galliformes; Phasianidae;				
TITLE	Phasianine; Gallus.				
JOURNAL	1 (bases 1 to 446)				
COMMENT	Murray,F. BP Chicken Brain Library Unpublished (2001) Contact: Frazer Murray Dept. Genomics and Bioinformatics Roslin Institute Roslin, Midlothian, EH25 9PS, UK Tel: +44 (0)131 527 4200 Fax: +44 (0)131 440 0434 Email: frazer.murray@bbsrc.ac.uk GCGGCCCTTTTATTTTTTTTTTTTTT 3' Poly A RNA purchased from Clontech (*6854-				
FEATURES	Seq primer: T7. Location/Qualifiers				
source	1..446 /organism="Gallus gallus" /db_xref="taxon:9031" /clone="ROS065F10" /clone_lib="BP Chicken Brain Library" /tissue_type="Brain" /dev_stage="Unknown" /lab_host="DH10B" /note=Vector: pSPORT1; Site_1: NotI; Site_2: SalI. Cloned unidirectionally. Primer: Oligo dT. 5' adaptor sequence: 5' TGACCTCGAG 3'; 3' adaptor sequence: 5' GGGCCGCTTTTATTTTTTTTTTTTTT 3' Poly A RNA purchased from Clontech (*6854-1)"				
BASE COUNT	88 a 158 c 86 g 112 t 2 others				
ORIGIN					
Query Match	1.9%; Score 222.2; DB 9; Length 446; Best Local Similarity 75.6%; Pred. No. 8e-28;				
Matches 323; Conservative	0; Mismatches 80; Indels 24; Gaps 3;				
Oy 10787	ACGTTTCCTGCATCCATCATTAAGCCTTCCTCGTAGAGTTAGTCCATCCCTT	10846			
Dd 1	ACGTTTCCTGCATCACTAACCTAAACCCTCGTGCTAGTTTAAACA-TTCCCCTT	59			
Oy 10847	GTGCTATCACCTGCCTACTGTGTTAAAAGATGATTCTCCCTCTT-----	10892			
Dd 60	GGCGCTGTCACATTCACACCTTCTGGATACGCCCTCCCTTCTGTTTATAGCTCCCTTC	119			
Oy 10893	-----TGGAGGTTGCATAAGAGTCTCTGACGCTTCTCTCTCGAGATGANC	10946			
Dd 120	AAGTACTGGAAGGCACACATGAGAGTCTCCCTCGAGACTT---CTCTTCACAGCTAANA	176			
Oy 10947	AAGCCAGTCTCCCTCAGCTGTCTTTATGAGAGAGTGTCTCAGGCCCTGTATCAATCTT	11006			
Dd 177	ATGCCCCAGTCCCTCAACCTTTCTCTCAGAGAGAGTGTCTCAGGCCCTGTATCAATCTT	236			
Oy 11007	GTGGCCCTCTCTGAGCCGCTCAAGAGCTCCACATCTTCTCTACTGTGGGGCCCGC	11056			
Dd 237	GTGGCCCTCTCTGTGAGCCACATCTCAAGAGCTCCACATTTTCTCTAGCTGGGGCCCGG	296			
Oy 11067	GCCTGAATCACTACTCTCCAGATGGGGCCCTCAAAAAGCAGAGATTAAGAGGACATTCAC	11126			
Dd 297	GCCTGAGCAGCACTACTCCAGATGGGGCCCTCAAAAAGAGTGAATAGGGGCAATTCAC	356			

[illegible][illegible]

[illegible]

Query	7048	TGATGACGATCTTCAGATGGGCGCTTA	7075
Db	659	TGATGACGATCTTCAGATGAGGNTTCA	686
RESULT 8			
AM240181/c			
LOCUS	AM240181	489 bp	mRNA Linear EST 27-APR-2000
DEFINITION	ptlc.pk002.n15 chicken T cell cDNA library		Gallus gallus cDNA
ACCESSION	AM240181		
VERSION	AM240181.1	GI:6579921	
KEYWORDS	EST.		
SOURCE	chicken.		
ORGANISM	Gallus gallus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;		
	Phasianinae; Gallus.		
	1 (bases 1 to 489)		
REFERENCE			
AUTHORS	Morgan, R.		
TITLE	Chicken T cell ESTs		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robin Morgan University of Delaware Townsend Hall, Newark, DE 19717, USA Tel: 302-831-1341 Fax: 302-831-2822 Email: morgan@udel.edu Clones can be ordered online at http://www.chickest.udel.edu .		
FEATURES			
SOURCE	1..489		
	/organism="Gallus gallus"		
	/db_xref="taxon:9031"		
	/clone="ptlc.pk002.n15"		
	/clone_lib="chicken T cell cDNA library"		
	/sex="Male and Female"		
	/cell_type="splenic T cell"		
	/lab_host="E.coli DH10B"		
	/note="Vector: pB42AD"		
BASE COUNT	134 a 87 c 135 g 106 t	27 others	
ORIGIN			
Query Match	1.7%	Score 201;	DB 10; Length 489;
Best Local Similarity	67.7%	Pred. No. 3.1e-24;	
Matches 319; Conservative	0;	Mismatches 127;	Indels 25; Gaps 3;
QY 10660	CCAGATCTGACTGACGAGCAGCCGAGGCGTCCATCCAACTGGGCAT--GAACACC	10717	
Db 469	CCCAATTAAATATTGACACGAGTNGCCAGGCCCATCCAACTGACCTTTGAACATTT	410	
QY 10718	TCCAGGATGAGCATCCCAACCTCTCTGGGACGCTGTGCGCAGCACCTCACCACTC	10777	
Db 409	TCCAGGGACAGGNCATCCCAACTTTTGGGACGCTTTCACACCTTCACCACTT	350	
QY 10778	TCTGTGAGAACCTTTCCCTCGATCCCAATCAATCAACCTTCCTCTGAGGTTAGATCA	10837	
Db 349	TNATGTGAAGACTTCCTNMAACATCCAACTTAATNTTCCCTCCCTCAACTTAACCA	290	
QY 10838	CTCCCTCTGTGCTATCACTGCTACTCTGTGTAAGAGTTGATTCCTCTCTTT--	10892	
Db 289	TTTCCCTGTGTCNTGTTGTATCTACCTTNCMAAGAGCTGACCTCCCTCMTGTTATAG	230	
QY 10893	-----TGAAGTTTGCATGAGGTCTCTTGACAGCTTCTCTCTTCC	10937	
Db 229	GCTCCCTTAGGTANTGAAGGTTGCAATTAGTACCCGGCAACTTTT--TCTTC	173	
QY 10938	AGGATGAACAAGCCAGCTCCCTCAGCCTGTATATAGAGAGGTGCTCCAGCCCTGTG	10997	
Db 172	GGGTTGAACAAGCCAGCTCCCTCAGCMTGTTTGTAGGGAGGTGCTCCAGCTTTTG	113	
QY 10998	ATCATCTTTGTGGCCCTCTCTGGAACCCGCTTCAAGAGCTCCACATCTTTCCTGTACTGG	11057	

QY	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	BASE COUNT	ORIGIN
Db	112	ATCATCTTTGAGCCCTGNTNGATCTCCGACACAGNTCCGCTTTTNTGTAAAG	53												
QY	11058	GGGCCCCGAGCCTGTAATGACGACTCTCCGATGAGGGCCCTCAAAAGACGACAG	11108												
Db	52	GGGGCTCCAGACCTTGACACAGTACTCCAGAAAGGCCACAGGACAGAG	2												
RESULT 9															
LOCUS	AJ445833		700 bp	mRNA	linear	EST	19-Apr-2002								
DEFINITION	AJ445833	riken1 Gallus gallus cdna clone 11j14r1, mRNA sequence.													
ACCESSION	AJ445833														
VERSION	AJ445833.1	GI:20213054													
KEYWORDS	EST.														
SOURCE	Chicken.														
ORGANISM	Gallus gallus														
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;														
AUTHORS	Archosaustra; Aves; Neognathae; Galliformes; Phasianidae;														
TITLE	Phasianinae; Gallus.														
JOURNAL	1 (bases 1 to 700).														
COMMENT	Buerstedde, J.M.														
FEATURES	Gallus gallus bursal lymphocyte EST														
SOURCE	unpublished (2002)														
CONTACT	Contact: Buerstedde JM														
CELLULAR	Cellular Immunology														
HEINRICH	Heinrich-Pette-Institute														
MARTINSTR.	Martinstr. 52, 20251 Hamburg, Germany														
EMAIL	Email: URL: http://genetics.hpi.uni-hamburg.de/dt40est.html.														
LOCATION	Location/Qualifiers														
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/clone_lib="riken1"															
/clone_type="bursal lymphocyte"															
/dev_stage="2-3 weeks old"															
/note="CB inbred strain"															
Query Match	1.7%	Score 197.4;	DB 9;	Length 700;											
Best Local Similarity	68.5%	Pred. No. 1.1e-23;													
Matches 316;	Conservative 0;	Mismatches 141;	Indels 4;	Gaps 3;											
QY	10724	GATGAGCATCCACACACCTCTCTGTGGGAGCCCTGTGCCACAGACTTCA-CCACCTCTCTGT	10782												
Db	1	GATGGGCATCATCAGCCCTCTGGACACCTCTTCCCGAGGGTCTCACCCACCTCTCAGT	60												
QY	10783	GAAAGACCTTTCGCCGATCAATCAATCAAGCTTCGCCCTTGAGAGTCAAGTCAACCTCC	10842												
Db	61	GGAAAACTTGGCCCTGACAT													

Db	418	CCACCCTCTTTTGTATGTAGCCACGAGGTACTGTCTCTGC	458
RESULT 10			
LOCUS	AJ456416	826 bp	mRNA
DEFINITION	AJ456416 riken1 Gallus gallus CDNA clone 818r1, mRNA sequence.		
ACCESSION	AJ456416		
VERSION	AJ456416.1	GI:20266512	
KEYWORDS	EST.		
SOURCE	chicken.		
ORGANISM	Gallus gallus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.		
REFERENCE	1 (bases 1 to 826)		
AUTHORS	Buerstedde, J.M.		
TITLE	Gallus gallus bursal lymphocyte EST		
JOURNAL	Unpublished (2002)		
COMMENT	Contact: Buerstedde JM Cellular Immunology Heinrich-Pette-Institute Martinistr. 52, 20251 Hamburg, Germany Email: URI: http://genetics.hpi.uni-hamburg.de/dt40est.html .		
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	/note="CB Inbred strain"		
BASE COUNT	191 a 234 c 160 g 240 t	1	others
ORIGIN			
Query Match	1.7%; Score 197.4; DB 9; Length 826;		
Best Local Similarity	68.5%; Pred. No. 9,8e-24;		
Matches 316; Conservative	0; Mismatches 141; Indels 4; Gaps 3;		
Oy 10724	GATGAGCATCCACACACCTCTCTGTGGGACGCTGTGCCACACCTCA-CCACCCCTCTCTGT	10782	
Db 1	GATGGCCCATCCACACGCTCTGTGACACACCTGTCCCGAGGCTCTCACCCACCTCTCTAGT	60	
Oy 10783	GAGAGACCTTTTCCCGATCCATCCATGAAGCTCCCTGAGGTAGATCCACCTCC	10842	
Db 61	GGAAAACTTTTGCTCGACATCTAATCTAATTTTCCCTCTTGAATTAAACTATTTCTT	120	
Oy 10843	CCCTGTGCTATCACTGTCTACTCTCTGTAAAAAGTTGATTCTCTCTTTTGGAGAGTTG	10902	
Db 121	CCCTGTTCGATTTGCTGTCTTTAAAAAATAAAATTTCTCTTGTATTAATATTC	180	
Oy 10903	CATGAGGTCTCTTGACGCTTCTTCTCTCTGTGACAGATTAACAAGCCGACGCTCCCTCA	10962	
Db 181	CCCTTAAGTATTTGGTAGGCATTAACAAGTCTCCCAACAGTCAAGCCAGCAGCTTCTCA	240	
Oy 10963	GCCCTGCTTTTATAGAGAGGGGCTCCACGCTCCGATCATGTTTGGCCCTCCCTGGA	11022	
Db 241	GCTGTCTTTCAATAGAGAGATGTCTCCACCTTCTCATATCTTGTGTGGCCCTCTC-AGA	299	
Oy 11023	CCCGTCCCAAGAGCTCCACATCTTCTCTGATCTGGGGGCCCCAGGCTCGAATGCACTACT	11082	
Db 300	CCCTCTCCAAAAGCTCAATATCTT--CTGTGTGAGTGGGCCCAAGCTCGATGCACTAGCA	357	
Oy 11083	CCAGATGGGGCCCTCAAAAAGACAGTAAAGAGGAGACATACCTTCTCAACCTGCTGG	11142	
Db 358	CCAGATGGGGCCCTCAATATGAGTGAAGAGAGGATGCTCACTCCCTCATCCAGCTGG	417	
Oy 11143	CCAGCCCTTTCTGTGAGGCTGGATCAACAAGGCTTTG	11183	
Db 418	CCACCTCTTTTGTATGTAGCCACGAGGTACTGTCTCTGC	458	

```

RESULT 11
LOCUS      GGA246112/c      914 bp      DNA      linear      GSS 21-JUN-1999
DEFINITION Gallus gallus anonymous sequence from cosmid mapping to chromosome
6 (Cosmid 56 - Contig 3), genomic survey sequence.
ACCESSION  AJ246112
VERSION     AJ246112.1  GI:5139449
KEYWORDS    GSS: genome survey sequence.
SOURCE      Gallus gallus
ORGANISM    Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Phasianidae; Gallus.
REFERENCE   1 (bases 1 to 914)
AUTHORS     Smith,J., Bruley,C.K., Paton,I.R., Law,A.S., Masabanda,J.,
Maddington,D., Fries,R. and Burt,D.W.
TITLE       Integration of the genetic and physical maps of the chicken
macrochromosomes
JOURNAL     Unpublished
REFERENCE   2 (bases 1 to 914)
AUTHORS     Law,A.S.
TITLE       Direct Submission
JOURNAL     Submitted (14-JUN-1999) Law A.S., Division of Molecular Biology,
Roslin Institute, Roslin, Midlothian EH25 9PS, Scotland, UK
FEATURES
SOURCE      1..914
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             /db_xref="taxon:9031"
             /chromosome="6"
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BASE COUNT  281 a      179 c      208 g      246 t
ORIGIN
Query Match      1.6%; Score 193.2; DB 17; Length 914;
Best Local Similarity 78.0%; Pred.No.4.8e-23;
Matches 259; Conservative 0; Mismatches 68; Indels 5; Gaps 2;

QY 10533 CTGGGGCTCCAGATTAGTGTAAACCTACTTATACATCATCAATATCATGATGGCC 10592
DB 643 CTGGACTCTTCATAGAGTGTCAAGTATTCACAACAATCAACAATACGGAATGGCC 584
QY 10593 TGGTTTGAAGGAGCCCAAGAGATCATGAAGATCCAAACACCCGCCAGAGGAGCA 10652
DB 583 TGGTTTGAAGGAGCTCAAGATATGATGAGCTCCAAACCCCTGCG--CAGCAGAGGCA 526
QY 10653 CCAACCTCCAGATCTGTAGTACAGCAGGAGCCAGGCTCCATCCAACTGGGCCATGA 10712
DB 525 CCAGTCTCCCAT--TTACTAGACCAAGTTGCCAGGAGCTCATCCAACTGGCCTTGA 469
QY 10713 ACACCTCCAGAGATGAGACATCCAACTCTCTGGGCGAGCTGTGCCAGCCTCACC 10772
DB 468 ACACCTCCAGAGGAGGAGCTCCAACTCTCTGGGCGAGCTGTGCCAGCCTCACC 409
QY 10773 CCCTCTCTGTGAAGACTTTTCCCTGACATCCATCAATCAAGCTTCCCTGGAGTTAG 10832
DB 408 CTCTCTCTGTGAAGAACTCTCTCCCTGACATCCAACTTAATCTCCCTTTCAAGTTAA 349
QY 10833 ATCCACTCCCTCTGTGTATCAGTCTACT 10864
DB 348 AACCGTCCCTCTGTGTATCAGTCTACT 317

RESULT 12
LOCUS      BG624980      437 bp      mRNA      linear      EST 18-APR-2001
DEFINITION Bg624980
              pgnlc.pk001.b3 Normalized chicken lymphoid cdna library gallus
              gallus cdna clone pgnlc.pk001.b3 5' similar to p1f150209|150209
              reverse transcriptase VtgTII, pol-I like - chicken (fringet)
              gblAA58720.11 (M28069) unknown protein [Gallus gallus]g, mRNA
              sequence.
ACCESSION  BG624980
VERSION    BG624980
ORIGIN     BG624980.1  GI:13675493

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KEYWORDS    EST.
SOURCE      chicken.
ORGANISM    Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianidae; Gallus.
REFERENCE   1 (bases 1 to 437)
AUTHORS     Morgan,R.W. and Burnside,J.
TITLE       Chicken Lymphoid ESTs
JOURNAL     Unpublished (2001)
COMMENT     Contact: Robin W. Morgan
              University of Delaware
              Townsend Hall, Newark, DE 19717, USA
              Tel: 302-831-1341
              Fax: 302 831-2822
              Email: morganudel.edu, www.chickest.udel.edu.
FEATURES
SOURCE      1..437
             /organism="Gallus gallus"
             /db_xref="taxon:9031"
             /clone="pgnlc.pk001.b3"
             /clone_lib="Normalized chicken lymphoid cdna library"
             /sex="Male and Female"
             /tissue_type="thymus, bursa, spleen, PBL, bone marrow"
             /lab_host="E.coli EMDH10B"
             /note="Vector: pCMVSPORT 6"
BASE COUNT  110 a      80 c      119 g      107 t      21 others
ORIGIN
Query Match      1.6%; Score 191; DB 12; Length 437;
Best Local Similarity 78.2%; Pred.No.1.6e-22;
Matches 241; Conservative 0; Mismatches 66; Indels 1; Gaps 1;

QY 10578 AATCATAGATGGCTGGTTGGAAGGAGCCCAAGATCATGAAGATCAACACCCCG 10637
DB 307 ACTTATAGATGGCTGGTTGGAAGGAGCTCAAGATCATGAAGATCAACACCCCGN 248
QY 10638 CCACAGCGGGGCCCAACACCTCCAGATCTGTACTAGCCAGGAGCCAGGCGCTCAT 10697
DB 247 TGTGCTGACGGGCGACCACTTCCACATTTATCTAGATCAGCTGCGGAGGCTTCAT 188
QY 10698 CCAACCTGGCGCATGAACACCTCCAGGATGAGATCCACACACCTCTGGGAGCCTGT 10757
DB 187 CCAACCTGGCGCTTGAACATTTGAAGGATGGGAGATCCACACCTCTGTGGGAGCCTGT 128
QY 10758 GCCAGACCTCACACCTCTCTGTGAGAGACTTTTCCCTGACATCCAACTTAAGCCTTC 10817
DB 127 TCCAGACCTCACACCTCTCATAGTAAAGTACTTCCCGGCTATCCAACTAA--TCTTC 69
QY 10818 CCTCTGTAGTTAGTATCCACCTCCCTGTGCTATCACTGTCTACTCTGTGTAAGAGTT 10877
DB 68 CCTCTGTAACTTAAGAACATTTCTCTGTCTGTATCTGCTTCAAGAGTT 9
QY 10878 GATTCTCC 10885
DB 8 GGCTCTCC 1

RESULT 13
LOCUS      GG0000392/c      608 bp      DNA      linear      GSS 07-SEP-2001
DEFINITION Gallus gallus GSS sequence, clone 901C17bH2, genomic survey
sequence.
ACCESSION  AL605912
VERSION    AL605912.1  GI:15552150
KEYWORDS    GSS: genome survey sequence.
SOURCE      chicken.
ORGANISM    Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianidae; Gallus.
REFERENCE   1 (bases 1 to 608)
AUTHORS     Clark,M.S., Edwards,Y.J., McQueen,H.A., Meek,S.E., Smith,S.,

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REFERENCE	1 (bases 1 to 581)
AUTHORS	Porter,T.E. and Cogburn,L.A.
TITLE	ESTs from Primary Chicken Pituitary/Hypothalamus/Pineal
JOURNAL	library USDA/IRAFs Animal Genome Project
COMMENT	unpublished (2001)
	Contact: Larry A. Cogburn

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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 27, 2003, 03:56:02 ; Search time 1658 Seconds
(without alignments)
16224.439 Million cell updates/sec

Title: US-09-922-549B-67
Perfect score: 11945
Sequence: 1 tgcgcctctcttgatattc.....tgcgcctctgctcttaggg 11945

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 segs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 100%
Listing first 45 summaries

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- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	142	1.2	22268	ABQ88219	Human osteoblast d
2	129.4	1.1	23653	ABK14793	Platelet-derived g
3	87.2	0.7	792	AAO36054	Human nov gene p
4	86	0.7	385	ABN79468	Human ORF4415 cDNA
5	85	0.7	6644	AAK33181	Base sequence of t
6	85	0.7	7372	AAK33182	Base sequence of t
7	85	0.7	7797	AAK33180	Cowpox virus bst
8	85	0.7	7996	AAK33184	Base sequence of t
9	83.4	0.7	6668	ABL33697	Human immune syste

10	79	0.7	14006	ABL33958	Human immune syste
11	78.6	0.7	222	AAZ98517	Chicken egg white
12	78.2	0.7	583	AAQ63457	Chicken (egg white
13	77.6	0.6	97	AAE67697	Insulator plasmid
14	75.6	0.6	7442	AA54668	Tumour suppressor
15	74.6	0.6	6216	AAV01425	Plasmid pRC/ASR-S
16	74.2	0.6	6024	ABL33647	Human immune syste
17	74.2	0.6	9539	AA545347	Chemically pretrea
18	74.2	0.6	6292	ABK28180	DNA transcription
19	73	0.6	6292	AA546735	Tumour suppressor
20	72	0.6	6419	ABL33267	Human immune syste
21	71.4	0.6	6898	ABN80222	Human chemically m
22	71.4	0.6	7814	AA546530	Tumour suppressor
23	71	0.6	6668	ABL33696	Human immune syste
24	71	0.6	8298	ABN80191	Human immune syste
25	70.4	0.6	7571	ABL33527	Human chemically m
26	70.4	0.6	12237	ABL33358	Human immune syste
27	70	0.6	15548	ABL34155	Human immune syste
28	69.8	0.6	34769	AA546774	Tumour suppressor
29	69.6	0.6	6767	AA546608	Tumour suppressor
30	69.2	0.6	16033	ABL33404	Human immune syste
31	68.4	0.6	7597	ABL33013	Human immune syste
32	68	0.6	5986	AA545438	Chemically pretrea
33	68	0.6	5986	ABK28287	DNA transcription
34	68	0.6	6048	ABQ67002	Human angiogenesis
35	68	0.6	21537	ABL33999	Human immune syste
36	67.8	0.6	6030	AA545456	Chemically pretrea
37	67.8	0.6	6030	AA561348	Human gene regulat
38	67.8	0.6	6332	ABK28312	DNA transcription
39	67.8	0.6	6352	ABL32905	Human immune syste
40	67.8	0.6	8079	ABL92313	Chemically treated
41	67.4	0.6	6145	ABL32972	Human immune syste
42	67.2	0.6	887	AA194064	Human neuroblastom
43	67	0.6	863	AA195036	Human neuroblastom
44	66.6	0.6	866	AA194006	Human neuroblastom
45	65.8	0.6	822	ABQ44852	Oligonucleotide fo

ALIGNMENTS

RESULT 1	
ABQ88219/c	
ID	ABQ88219 standard; cDNA: 22268 BP.
XX	
AC	ABQ88219;
DT	18-SEP-2002 (first entry)
XX	
DE	Human osteoblast differentiation related cDNA seq ID NO 126.
XX	
KW	Human; osteoblast; stem cell differentiation; bone tissue deposition;
KW	osteoporosis; osteopathic; ss.
OS	Homo sapiens.
XX	
PN	WO200250301-A2.
PD	27-JUN-2002.
XX	
PF	18-DEC-2001; 2001WO-US48276.
XX	
PR	18-DEC-2000; 2000US-255882P.
XX	
PR	24-APR-2001; 2001US-285691P.
XX	
PA	(GENE-) GENE LOGIC INC.
PA	(PROC) PROCTER & GAMBLE CO.
PI	Ji D, Axelrod DW, Cook JS, Jaiswal N, Einstein R, Houghton A;
PI	Mertz L;
XX	
DR	WPI; 2002-557663/59.
XX	

AC AAQ36054;
 XX
 DT 24-MAY-1993 (first entry)
 XX
 DE Chicken nov gene promoter sequence XXXV.
 XX
 XX avian nephroblastoma; avian myeloblastoma virus;
 KW stringent hybridisation; ss.
 XX
 OS Gallus domesticus.
 XX
 PN W09300430-A.
 XX
 PD 07-JAN-1993.
 XX
 PF 25-JUN-1992; 92MO-FR00589.
 XX
 PR 25-JUN-1991; 91FR-0007807.
 XX
 PA (CNRS) CENT NAT RECH SCI.
 XX
 PI Martinerie C, Perbal B;
 XX
 DR WPI, 1993-036377/04.
 XX
 PT Nucleotide sequences hybridising to regions of chicken nov gene -
 PT useful as probes for detecting complementary sequences to
 PT evaluate development and/or differentiation of tumours
 XX
 PS Disclosure: Page 49-50; 67pp; French.
 XX
 CC The invention includes nucleotide sequences which can hybridise to
 CC all or part of the chicken nov gene under stringent conditions
 CC (i.e. 50% formamide, 5 x SSC). The promoter sequence from the
 CC chicken nov gene, contained in a 1kb SmaI-XhoI fragment and
 CC comprising consensus sequences for different transcription factors
 CC such as Ap2 and Sp1 is specifically disclosed. It also comprises
 CC NF kappa B2 and factor NFkB binding sites.
 XX
 SQ Sequence 792 BP; 158 A; 188 C; 285 G; 161 T; 0 other;

Query Match 0.7%; Score 87.2; DB 14; Length 792;
 Best Local Similarity 57.8%; Pred. No. 2.4e-10;
 Matches 259; Conservative 0; Mismatches 168; Indels 21; Gaps 5;

OY 10650 CCACCAACCTCCAGATCTGTACTATACACGACGCGGCGTCCATCCACTGCGCA 10709
 DB 440 CAACCATCCCTACATTTCTCACTAACCACATCCCTCAGTGCACATCTACACGTTTCC 381
 OY 10710 TGAACACCTCCAGGATGAGCATCCACAACCTCTCTGGGACAGCTGTGCACACCTCA 10769
 DB 380 TGAACATCTCCAGGATGAGTATCC--ACCTCGCTGGGACACATCTGACATATACCTCA 324
 OY 10770 CCACCTCTCTGTG--AAGAACTTTCCCTGACATCCATCTAGCCCTTCCCTGTGAG 10827
 DB 323 CCATTTTGGGAGAAAAAATTTGTTCTGATATCCAAACTGAAATCCCTCGGACATTA 264
 OY 10828 GTTAGATCCATCCCTCTGTGCTATCAGTGTACTCTTGTAAAGTTGA----- 10879
 DB 263 TTTAACACAGTTTCTCTATCTATCACTGATACCTGGAGACAGAGCCGACCTCCACC 204
 OY 10880 --TTCTCTCTTTTGGAGAGTTGCAATGAGGCTCTTGACGCTTCTTCTCTCTGCG 10937
 DB 203 TCACCAACACCTCTCCAGGAGATTTTAAAGACAATATATGTTTCCGAGACCTCTCC 144
 OY 10938 AGATATGAACAGCCAGCTCCCTCAGCCTGTCTTTATAGAGAGGCTCTCCAGCCCTCTG 10997
 DB 143 GGAAGCTAAACATCCAACTTCTCAGCTGCTTCCAAATGAACATGCTCCACACTCTC 84
 OY 10998 ATATCTTTTGGCCCTCTCTGACCCGCTCAAGAGCTCCACATCTTCTCTGTACTGG 11057
 DB 83 ACCAC--TCGTCCCTTCTCTGTGACACACTCCATGGCCCTCGA-----TGTCTTGTAGTGA 30

OY 11058 GGGCCCCAGGCGTGAATGCAGTACTCCA 11085
 DB 29 GGGGCCCAAACTGAACACAGCACTCGA 2

RESULT 4
 ABN79468/C
 ID ABN79468 standard; cDNA: 385 BP.
 XX
 AC ABN79468;
 XX
 DT 08-JUL-2002 (first entry)
 XX
 DE Human ORF4415 cDNA, SEQ ID NO:8829.
 XX
 KW Human; ORF; open reading frame; ORFX; drug screening; diagnosis;
 KW disease monitoring; cytokine; cell proliferation; cell differentiation;
 KW immune modulation; haematopoiesis regulation; tissue growth;
 KW angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
 KW thrombolytic; tumour inhibition; bodily characteristics; fertility;
 KW behaviour; cancer; proliferative disorder; neurological disorder;
 KW cardiovascular disease; immune system disorder; organ transplantation;
 KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
 KW hypothyroidism; cholesterol ester storage disease; infection; vulnery;
 KW vasotropic; antipsoriatic; antidiabetic; cyostatic; nootropic;
 KW neuroprotective; antithrombotic; anticoagulant; thrombolytic;
 KW cardiant; hypotensive; antihypertoid; antiinflammatory; immunomodulator;
 KW dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200190366-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 24-MAY-2001; 2001WO-US17076.
 XX
 PR 24-MAY-2000; 2000US-206690P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Leach MD, Shinkets RA;
 XX
 DR WPI: 2002-106200/14.
 XX
 PT P-PSDB; ABP35442.
 XX
 PT Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and disorders related to organ
 PT transplantation -
 XX
 PS Claim 1: Page 2450; 2508pp; English.

Sequences ABP31028-ABP35561 represent 4534 novel human proteins
 designated ORF (open reading frame) 1-4534, and sequences ABN75054-
 CC ABN79587 represent cDNAs encoding them. The invention also encompasses
 CC polypeptides at least 80% identical to the ORF1-ORF4534 (collectively
 CC referred to as ORFX) proteins, polynucleotides at least 85% identical to
 CC the ORFX nucleic acid sequences, vectors and host cells comprising ORFX
 CC polynucleotides, the recombinant production of ORFX proteins, antibodies
 CC specific for ORFX proteins, methods of detecting ORFX polynucleotides and
 CC polypeptides, methods of screening individuals for a predisposition to an
 CC ORFX-associated disorder. The ORFX proteins of the invention have a wide
 CC range of biological activities, such as cytokine, cell proliferation,
 CC cell differentiation, immune modulation, haematopoiesis regulation,
 CC tissue growth, angiogenesis, activin or inhibin activity, chemotactic/
 CC chemokinetic activity, haemostatic activity, thrombolytic activity,
 CC receptor/ligand, antiinflammatory activity, tumour inhibition activity,
 CC and antineoplastic activity, and may also be involved in the determination
 CC of bodily characteristics, fertility and behaviour. ORFX proteins,
 CC nucleic acids and antibodies may be used in the treatment of cancers,
 CC other proliferative disorders such as psoriasis and benign tumours,

CC neurological disorders such as epilepsy and Alzheimer's disease,
CC cardiovascular diseases, immune system disorders, disorders related to
CC organ transplantation, disorders of tissue growth and regeneration,
CC diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester
CC storage disease, and infectious diseases caused by viral, bacterial,
CC fungal and other pathogens. ORFX nucleic acids may also be used as a
CC source of primers and probes, in the detection of ORFX genomic sequences
CC or transcripts, in the identification and cloning of homologous
CC sequences, in genetic diagnosis, and in forensic biology. The ORFX
CC nucleic acids may additionally be used to produce transgenic animals
CC which may be useful for studying the function and/or activity of ORFX
CC protein, and in drug screening. The ORFX proteins may also be used as
CC immunogens to generate specific antibodies, which are useful in the
CC diagnosis, treatment and monitoring of ORFX-associated diseases.

SQ Sequence 385 BP; 100 A; 83 C; 98 G; 99 T; 5 other;

Query Match 0.7%; Score 86; DB 24; Length 385;

Best Local Similarity 69.5%; Pred. No. 3.1e-10;

Matches 116; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

DB 11046 TTCCTGACTGGGGCCCGCCAGGCTGAATGAGTCCAGATGGGGCTCAAGAGCA 11105

DB 365 TCCTGTGCTGGGGCCCGCCAGTGAATGAGTCCAGATGGGGCTCAAGAGCA 306

QY 11106 GAGTAAAGAGGACAAATCACTTCTCTGAGCCGCTTCTGATGAGCC 11165

DB 305 AATTAGAGAAACAAATCACTTCTCTGAGCCGCTTCTGATGAGCC 246

QY 11166 TGGATCAACACTGGCTTCTGAGCTGCAACTTCTCTATCACTTCA 11212

DB 245 AGGATACAGTTGGCTTCTGATGAGCAACACTGGCAACTCA 199

RESULT 5

AA33181/c

ID AA33181 standard: DNA: 6644 BP.

XX AA33181;

DT 25-JUN-1999 (first entry)

DE Base sequence of the plasmid prx-ires-bsr.

KW Cowpox virus: bsr; viral vector; expression; apoptosis; resistance;
KW crma; bcl-2; bcl-x1; FlIP; survivin; IAP; ILP; adenovirus; cancer;
KW autoimmune disease; graft rejection reaction; inflammation;
KW inflammatory disease; ss.

XX Synthetic.

OS Cowpox virus.

PN WO9913073-A2.

PD 18-MAR-1999.

PE 07-SEP-1998; 98WO-JP04010.

PR 08-SEP-1997; 97JP-0259235.

PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.

PI Hamada H;

DR WPI; 1999-243728/20.

XX New apoptosis-resistant virus-sensitive cell

XX Example 1; Page 38-41; 51pp; English.

CC The present invention describes an apoptosis-resistant virus-sensitive
CC cell line into which an apoptosis resistance gene has been introduced.
CC The recombinant viruses generated are capable of expressing apoptosis-

CC associated genes. These can then be used in a variety of diseases for
CC which the induction of apoptosis by gene transfer, or where the
CC inhibition of harmful apoptosis, is therapeutic. The recombinant viruses
CC are useful as vectors for gene therapy which can be applied to cancer
CC therapy for destroying cancer cells selectively, the treatment of
CC autoimmune diseases and graft rejection reaction, and apoptosis induction
CC therapy for inflammatory cells in inflammatory diseases. Prior arts have
CC encountered the problem where if an adenovirus vector capable of
CC expressing an apoptosis-associated gene is introduced into animal cells,
CC the cells producing the virus will be destroyed because the period of
CC time required to induce cell death by apoptosis is shorter than that
CC required to replicate and produce the virus, resulting in failure to
CC obtain a recombinant virus having the integrated apoptosis-associated
CC gene. In this invention an apoptosis-resistant 293 cell line (having an
CC apoptosis resistant gene introduced) is established and overcomes the
CC problem. The present sequence represents the base sequence of the
CC plasmid prx-ires-bsr, which contains the cowpox virus bsr gene, and
CC is used in an example from the present invention.

SQ Sequence 6644 BP; 2166 A; 1573 C; 1424 G; 1481 T; 0 other;

Query Match 0.7%; Score 85; DB 20; Length 6644;

Best Local Similarity 45.2%; Pred. No. 2.5e-09;

Matches 313; Conservative 0; Mismatches 360; Indels 0; Gaps 0;

QY 226 TTTTGTGCTGTTTTTTTTTTTTTTTTTTTTTAACTAGCTGTTTTCTTACT 285

DB 4398 TTTTGTGCTGTTTTTTTTTTTTTTTTTTTTTAACTAGCTGTTTTCTTACT 4339

QY 286 AATTTTCTAGCTGATGATTTTGCAGCTGAGAAATTTCTTCAAGAAAGAAC 345

DB 4338 TTTTGTGCTGTTTTTTTTTTTTTTTTTTTTTAACTAGCTGTTTTCTTACT 4279

QY 346 TTTTGTGCTGTTTTTTTTTTTTTTTTTTTTTAACTAGCTGTTTTCTTACT 405

DB 4278 TTTTGTGCTGTTTTTTTTTTTTTTTTTTTTTAACTAGCTGTTTTCTTACT 4219

QY 406 TGGTCTGATGATGAGAAACGTTGAGCACTGAGTTTATATAGTGTG 465

DB 4218 TTTTGTGCTGTTTTTTTTTTTTTTTTTTTTTAACTAGCTGTTTTCTTACT 4159

QY 466 GCTTGAAGCTGAGTACGCTGTTTCTTCACTGCTTCTGCTGCAATGCTT 525

DB 4158 TTTTGTGCTGTTTTTTTTTTTTTTTTTTTTTAACTAGCTGTTTTCTTACT 4099

QY 526 ATGCTTATTTTCCCTTGAAGTACGAGCTGCTGTTTTTCCCTTGAAGCTG 585

DB 4098 TTTTGTGCTGTTTTTTTTTTTTTTTTTTTTTAACTAGCTGTTTTCTTACT 4039

QY 586 GTGAGCTTATTTTCTAATGGATTTTACCTGATGATGATGATGATGAT 645

DB 4038 TTTTGTGCTGTTTTTTTTTTTTTTTTTTTTTAACTAGCTGTTTTCTTACT 3979

QY 646 GCTTGAATGTTTTCTTGAATGATGATGATGATGATGATGATGATGATGAT 705

DB 3978 TTTTGTGCTGTTTTTTTTTTTTTTTTTTTTTAACTAGCTGTTTTCTTACT 3919

QY 706 TTTTGTGCTGTTTTTTTTTTTTTTTTTTTTTAACTAGCTGTTTTCTTACT 765

DB 3918 TTTTGTGCTGTTTTTTTTTTTTTTTTTTTTTAACTAGCTGTTTTCTTACT 3859

QY 766 TTTTGTGCTGTTTTTTTTTTTTTTTTTTTTTAACTAGCTGTTTTCTTACT 825

DB 3858 TTTTGTGCTGTTTTTTTTTTTTTTTTTTTTTAACTAGCTGTTTTCTTACT 3799

QY 826 TATTTATGATTTTATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 885

DB 3798 TTTTGTGCTGTTTTTTTTTTTTTTTTTTTTTAACTAGCTGTTTTCTTACT 3739

QY 886 AATTTCTAGAGGATGCTGATGAGGCGGT 918

DB 3738 GCACTGCAAGAGGTTTATGATACAGCGGT 3706

[illegible]

QY	346	TTTTGGAAACGTACACCCCTTTCTTCAATCCCTTTTGCTTGTGCGCAATGCCCT	405
Db	5006	TT	4947
QY	406	TGGTTCGATGCAATPANGAAAACGTGATCGGAACTTGAGCTTTTATATAGTGTG	465
Db	4946	TT	4887
QY	466	GCTTGAAGAGCTTGATGAGCTGTGTGACACAGATACCTATTTAACTTTAGCCAGCTTG	525
Db	4886	TT	4827
QY	526	ATGCTTATTTTTTCCCTTGAGAGTAGAGCGTCTCGGTTTTTTTCCTTGAACGTG	585
Db	4826	TT	4767
QY	586	GTGAGGCGTACATTTTCTCAATGGATTTTTCACGTGATGATCTGTGTCATACCAAT	645
Db	4766	TT	4707
QY	646	GCTGTGAATGCTTTTCCCTAGTAAACATGTTGATACCTGAGATTTACATGTTGATATAC	705
Db	4706	TT	4647
QY	706	TTTGATCATGCTGTTCTAGTAAAAATATAGCATTTATAGAAAATAGTAATCCTGATT	765
Db	4646	TT	4587
QY	766	TCTCTTTTTTTTATCTGATGCTGTGTGTGTACAGGTCAACAGACTTACTCTATTTT	825
Db	4586	TT	4527
QY	826	TATTTATGAAATTTTATATGACAGTCTGTCGTGGTCTTGTTGTAAGATACAGCCTT	885
Db	4526	TT	4467
QY	886	AAATTTCTAGACGATGCTCAGTAGCGGGT	918
Db	4466	GCAACTGCAGAGAGGGTTTATGTGATACACGGGT	4434
RESULT 7			
AAK33180/c			
ID	AAK33180 standard; DNA; 7797 BP.		
XX			
AC	AAK33180;		
XX			
DT	25-JUN-1999 (first entry)		
XX			
DE	Cowpox virus bsr full length gene sequence.		
XX			
KM	Cowpox virus; bsr; Viral vector; expression; apoptosis; resistance;		
KM	cmrh; bcl-2; bcl-xl; FLIP; survivin; IAP; ILP; adenovirus; cancer;		
KW	autoimmune disease; graft rejection reaction; inflammation;		
XX	inflammatory disease; ss.		
OS	Cowpox virus.		
XX			
PN	W09913073-A2.		
XX			
PD	18-MAR-1999.		
XX			
PF	07-SEP-1998; 98WO-JP04010.		
XX			
PR	08-SEP-1997; 97JP-0259235.		
XX			
PA	(RPRG-) RPR GENCELL ASIA PACIFIC INC.		
XX			
PI	Hamada H;		
XX			
DR	WPI; 1999-243728/20.		
XX			
PT	New apoptosis-resistant virus-sensitive cell		

ID	ABL33958	standard: DNA; 14006 BP.
XX	ABL33958	
AC	ABL33958;	
DT	26-MAR-2002	(first entry)
XX		
DE	Human immune system associated gene	SEQ ID NO: 1931.
XX		
XX	Human, immune system disease; cytosine methylation; antiasthmatic;	
XX	antiartherosclerotic; antianaemic; cytosolic; noctropic;	
KW	neuroprotective; anti-HIV; anticonvulsant; ophthalmological;	
KW	anthrpaumatic; antiarthritic; antidiabetic; antipsoriatic;	
KW	antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;	
KW	acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;	
KW	neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;	
KW	gene; ds.	
OS	Homo sapiens.	
XX		
PN	WO200200928-A2.	
XX		
PD	03-JAN-2002.	
XX		
PF	02-JUL-2001; 2001WO-EP07537.	
PR	30-JUN-2000; 2000DE-1032529.	
PR	01-SEP-2000; 2000DE-1043826.	
XX		
PA	(EPIC-) EPIDEMIOLOGY AG.	
XX		
PI	Olek A, Piepenbrock C, Berlin K;	
DR	WPI: 2002-130909/17.	
XX		
PT	Nucleic acid comprising fragment of chemically modified gene, useful	
PT	for diagnosis and treatment of diseases associated with abnormal	
PT	cytosine methylation	
XX		
XX		
XX	Claim 1: SEQ ID NO 1931; 32pp + Sequence Listing; German.	
CC	The present invention provides a number of human immune system associated	
CC	genes which are modified by the methylation of cytosines. The sequences	
CC	can be used in the diagnosis and treatment of immune system disorders,	
CC	including eye diseases such as retinopathy, neovascular glaucoma and	
CC	macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid	
CC	leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,	
CC	rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel	
CC	diseases. The present sequence is a gene of the invention.	
XX		
SO	Sequence 14006 BP; 3278 A; 155 C; 3257 G; 7313 T; 3 other:	
XX		
Query Match	0.7%;	Score 79; DB 24; Length 14006;
Best Local Similarity	45.4%;	Pred. No. 1e-07;
Matches 283; Conservative	0;	Mismatches 340; Indels 0; Gaps 0;
OY	222 GAGGTTTTTTCGCCGTTTTTTTTTTTTTTTTTTTAACTAAGGTCCTTTTTCT	281
DB	1872 GATTTTTTTCGAAAGTTCTGTTTTGTTTTTTTTTTTTTTTTTTTAATTTTTTTTTTTTTT	1931
OY	282 TAGTAATTTTCTAGACGTGTATGTTTTGACAGGTGAGAAACATTTCTGCAAAAGAG	341
DB	1932 TTTTATTTTTTTTTTTTTTTTTTTTTTTTATTTTTTTTTTTTTTTTTTTTTTTT	1991
OY	342 AACCTTTGGAACGTGTACAGCCCTTTCTCTTCATTCCTTTTCTCTGTCGCAATG	401
DB	1992 TTTTTTTTTTTTTTTTGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	2051
OY	402 CCTTGGTTCGATTCGATTATGAAAACGTGACCGAAGCTGAGGTTTTTATTTATG	461

D b	2052	TTT	2111
Q y	462	TGTGGCTGGAAGCTTGAGACTGTGTTACACGAGATCACTTATTAAGTTBAGCAG	521
D b	2112	TT	2171
Q y	522	CTTGACCTTAAATTTTCCTTGAAGTAGAGCGCTCTCGGTTTTTTCCCTTGAA	581
D b	2172	TT	2231
Q y	582	ACGTGAGGCTBAGATTTTCTAATGGATTTTTACCTGATGATCTBAGTGCATACC	641
D b	2232	ATTTTTTTTTTTTCGTT	2291
Q y	642	AAATGCTGTAAAGTTTCCATGTAACAAGTGTGATCTCGGATTAACATGTTGAT	701
D b	2292	TTTTTTTTTTTCGTTTTTTTTTTTTTTTTTTTTTTTTTTATAATTTTTTTTTTTTTTT	2351
Q y	702	ATACCTGCATCTGTGTTCTACATAAATAATGATTTATAGAAATAGCATATTCCT	761
D b	2352	TTTTTTTTTTTTTTTTTTTTTTTTTTATTTGGATTTTTTTTTTTTTTTTTTTTTTTTTT	2411
Q y	762	GATTTCCTTTTTTTTATACCTCAAGCTCTGTGCTGACAGCTCAACAGACTTCACTCTA	821
D b	2412	TT	2471
Q y	822	TTTTTATTTATAGAATTTTAT 844	
D b	2472	TTTTTTTTTTTTTTTTTTTTTAT 2494	

	RESULT 11
ID	AA298517
XX	AA298517 standard; cDNA; 222 BP.
AC	AA298517;
DT	19-JUN-2000 (first entry)
DE	Chicken egg white Lysozyme gene 5' flanking and exon 1 fragment.
KM	DNA fixation; genetic engineering; medicine; pharmaceutical; chicken;
KW	DNA support; egg white; lysozyme; ss.
OS	Gallus sp.
XX	
PN	EP987335-A2.
XX	
PD	22-MAR-2000.
XX	
PF	02-SEP-1999; 99EP-0117273.
XX	
PR	04-SEP-1998; 98JP-0250619.
XX	
PA	27-AUG-1999; 99JP-0240910.
XX	
PA	(RIKA) INST PHYSICAL & CHEM RES.
XX	
PI	(HAYA/) HAYASHIZAKI Y.
XX	
DR	Hayashizaki Y;
XX	
PT	WPI; 2000-239224/21.
XX	
PT	Fixing nucleic acid to a support sheet, useful for preservation and to
XX	facilitate distribution, by applying as solution, particularly by
XX	printing, then drying -
PS	
XX	Disclosure; Fig 3; 13pp; English.
CC	
CC	The invention relates to a method for fixing DNA that comprises applying
CC	a DNA solution, optionally by printing, to a sheet-like support of
CC	determined thickness, then drying the solution. The fixed DNA (or
CC	other nucleic acid) is used in genetic engineering, biology, medicine
CC	and pharmaceuticals. The method allows prompt, efficient and simple

CC preservation of DNA on the support and allows simple distribution of the
 CC supported DNA through the mail. The sheets can be stored at normal
 CC temperatures, eliminating the need for low temperature storage of frozen
 CC aqueous solutions or glycerol-containing stock solutions. The DNA
 CC solution may be applied using a standard ink-jet printer, simply by
 CC replacing the ink cartridge with one containing the DNA solution. Very
 CC many DNAs, e.g. 1000, can be attached to the same support so that a
 CC booklet of 100 sheets will contain the complete set of murine cDNAs.
 CC The present sequence represents a chicken egg white lysozyme cDNA
 CC fragment. This is used in demonstrating a typical support sheet
 CC carrying lysozyme cDNA as a series of dots, which may be cut out
 CC individually. The sheet also contains sequence and structural information
 CC for lysozyme.

CC Sequence 222 BP; 44 A; 50 C; 65 G; 63 T; 0 other;

Query Match 0.7%; Score 78.6; DB 21; Length 222;
 Best Local Similarity 95.3%; Pred. No. 1.4e-08;
 Matches 81; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 11861 GCAGTCCCGCTGTGTACAGACATGCGCAATGAGGCTTGTCTAATCTGTGCTTTG 11920
 DB 1 GCAGTCCCGCTGTGTACAGACATGCGCAATGAGGCTTGTCTAATCTGTGCTTTG 60

OY 11921 CTTCTGCCCTGTGCTGCTTGAAGG 11945
 DB 61 CTTCTGCCCTGTGCTGCTTGAAGG 85

RESULT 12
 AA063457 standard; DNA; 583 BP.

XX AA063457;

DT 24-SEP-1994 (first entry)

DE Chicken (egg white) lysozyme gene.

KW Lytic peptide; resistance; fire blight; pomaceous fruit; scion;
 KW rootstock cultivar; transformation; transgenic variants; pears;
 KW apples; quinces; ss.

OS Chicken.

FH Key Location/Qualifiers
 FT CDS 30..470

ET /*tag= a

PN WO9407356-A.

PD 14-APR-1994.

PF 29-SEP-1993; 93WO-US09299.

PR 30-SEP-1992; 92US-0954347.

PR 18-MAR-1993; 93US-0033772.

PA (CORR) CORNELL RES FOUND INC.

PI Aldwinckle HS, Norelli JL;

DR WPI; 1994-135092/16.

DR P-PSDB; AAR53348.

PT Prod'n of transgenic pomaceous fruit with fire blight resistance -
 PT by transforming fruit scion or rootstock cultivars with a gene
 PT encoding a lytic protein, e.g. lysozyme

PS Disclosure; Page 38C; 61pp; English.
 CC Resistance to fire blight conferred on pomaceous fruit scion or
 CC rootstock cultivars can be induced by transforming the plant with a

CC gene encoding a lytic protein, e.g. lysozyme, cecropin, attacin or
 CC homologues. The transgenic variants show resistance to fire blight
 CC but retain their own characteristics. The method can be used to
 CC protect species of the Rosaceae family, e.g. pears, apples and
 CC quinces.
 CC See also AA063455-69.

CC Sequence 583 BP; 133 A; 168 C; 172 G; 110 T; 0 other;

Query Match 0.7%; Score 78.2; DB 15; Length 583;
 Best Local Similarity 96.4%; Pred. No. 2.9e-08;
 Matches 80; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 11863 AGTCCCGCTGTGTACAGACATGCGCAATGAGGCTTGTCTAATCTGTGCTTTGCT 11922
 DB 1 AGTCCCGCTGTGTACAGACATGCGCAATGAGGCTTGTCTAATCTGTGCTTTGCT 60

OY 11923 TCCTGCCCTGTGCTGCTTGAAGG 11945
 DB 61 TCCTGCCCTGTGCTGCTTGAAGG 83

RESULT 13

AAF67697 standard; DNA; 97 BP.

XX AAF67697;

DT 12-APR-2001 (first entry)

DE Insulator plasmid enhancer blocking sequence lys SPQ ID NO: 55.

KW Chicken; human; insulator; enhancer; DNA binding protein;
 KW gene expression; gene therapy; insulin-like growth factor-2; Igf2;
 KW knockout mouse; ds.

OS Unidentified.

PN WO200102553-A2.

PD 11-JAN-2001.

PF 19-APR-2000; 2000WO-US10509.

PR 30-JUN-1999; 99US-0141728.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Bell AC, West AG, Felsenfeld G;

DR WPI; 2001-091803/10.

PF Isolated DNA molecule useful for the regulation of gene expression and
 PF function in mammals and plants -

PS Example 1; Page 65; 96pp; English.

CC The present invention provides the sequence of a enhancer-blocking
 CC insulator from the chicken. Also provided are insulators from the murine,
 CC rat and human insulin-like growth factor-2 (Igf2) genes. The insulators
 CC can be used to modulate gene expression, for example in gene therapy and
 CC in knockout mouse production.

CC Sequence 97 BP; 22 A; 20 C; 23 G; 32 T; 0 other;

Query Match 0.6%; Score 77.6; DB 22; Length 97;
 Best Local Similarity 95.2%; Pred. No. 1.5e-08;
 Matches 80; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 9435 GAGGTTTACGTCATTGACATGAGAAATTGAGACCTCTACTGATAGCTATGTAAT 9494
 DB 5 GAGGCTTACGTCATTGACATGAGAAATTGAGACCTCTACTGATAGCTATGTAAT 64


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XX 13-MAR-1996; 96US-0013321.
XX
XX (SALA-) SOUTH ALABAMA MEDICAL SCI FOUND.
XX
XX PI Kayes SG;
XX
XX WPI; 1997-470644/43.
XX
XX PT Vaccine for schistosomiasis - comprising a non-integrating DNA
XX sequence encoding Schistosoma mansoni glutathione S-transferase
XX
XX PS Claim 4; Fig 7a; 57pp; English.
XX
CC A vaccine has been developed comprising a non-infectious,
CC non-integrating DNA sequence encoding Schistosoma mansoni
CC glutathione S-transferase (GST). The DNA comprises a plasmid
CC encoding a protein, polypeptide or peptide which is operably
CC linked to a promoter. The present sequence represents a
CC specifically claimed plasmid, pRC/ASK8-SmGST3. The vaccine
CC can be used for preventing or ameliorating the effects of
CC schistosomiasis infection. They elicit immunological responses
CC necessary for inducing resistance to infection and/or ameliorating
CC the disease in such as way as to alter subsequent transmission of
CC the disease.
XX
SQ Sequence 6216 BP; 1428 A; 1624 C; 1627 G; 1537 T; 0 other;

Query Match 0.68; Score 74.6; DB 18; Length 6216;
Best local Similarity 61.28; Pred. No. 7.6e-07;
Matches 139; Conservative 0; Mismatches 84; Indels 4; Gaps 1;

QY 10573 CATAGATCATAGATGGCTGGGTGGAGGAGGCCCAAGAGATGAGATCCACAC 10632
DB 432 CCTAGTATCATAGATGACAGGTGGAATACTTAAGATCATGAGTCCACCAT 373
QY 10633 CCCCAGCAGAGGAGGCCACCACTCCAGATCTGTAGACGAGCAGCCAGGAGC 10692
DB 372 GACCTAACCATACCTACTACTACTAC---AACCTCCGTTAATCATGTCCCGAGCAC 317
QY 10693 TCCATGCACTGAGCATGAGCATCCAGGATGAGCATCCAACTCTCTGGGAG 10752
DB 316 CACATCCAAACGGTTTAAAGACATCCAGGAGTGACATCAACACCTCCCTGGGGAG 257
QY 10753 CCTGTGCGACACCTCACACCTCTCTGTGAAGAACTTTCCCTGA 10799
DB 256 CCTATTCCAGTGTAAACACCTTTATGTAAAGATTTCCTGA 210

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OM nucleic - nucleic search, using sw model

Run on: March 27, 2003, 03:59:18 ; Search time 265 Seconds

(without alignments)
13823.600 Million cell updates/sec

Title: US-09-922-549b-67

Perfect score: 11945
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 segs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	80.2	0.7	222	4	US-09-388-917-1 Sequence 1, Appl
2	78.2	0.7	586	1	US-08-385-590A-3 Sequence 3, Appl
3	78.2	0.7	586	3	US-09-021-520-3 Sequence 3, Appl
4	62.6	0.5	7218	1	US-08-232-463-14 Sequence 14, Appl
5	56.4	0.5	1987	1	US-07-999-280A-23 Sequence 23, Appl
6	56.4	0.5	1987	1	US-08-426-036-23 Sequence 23, Appl
7	56.4	0.5	1987	1	US-08-426-279-23 Sequence 23, Appl
8	56.4	0.5	1987	1	US-08-401-013-23 Sequence 23, Appl
9	56.4	0.5	1987	3	US-08-426-570-23 Sequence 23, Appl
10	56.4	0.5	1987	3	US-08-426-243-23 Sequence 23, Appl
11	56.4	0.5	1987	3	US-08-401-632-23 Sequence 23, Appl
12	56.4	0.5	1987	2	US-08-487-826B-13 Sequence 13, Appl
13	54.6	0.5	19124	2	US-08-675-885-3 Sequence 3, Appl
14	53.4	0.4	974	3	US-09-363-708-3 Patent No. 5168051
15	49.2	0.4	2246	4	US-08-232-463-14 Sequence 14, Appl
16	49.2	0.4	2671	6	US-08-232-463-14 Sequence 14, Appl
17	48.8	0.4	7218	4	US-09-071-224-3 Sequence 3, Appl
18	48.6	0.4	1813	4	US-08-998-416-595 Sequence 595, Appl
19	48.2	0.4	658	4	US-09-465-558-53 Sequence 53, Appl
20	48.2	0.4	1206	4	US-08-897-340-4 Sequence 4, Appl
21	48	0.4	1700	2	US-09-252-329-4 Sequence 6, Appl
22	48	0.4	1700	3	US-08-628-417-6 Sequence 6, Appl
23	47.8	0.4	240	1	US-08-628-417-5 Sequence 13, Appl
24	47.4	0.4	140	1	US-08-628-417-5 Sequence 13, Appl
25	47.4	0.4	2252	4	US-08-334-179A-13 Sequence 13, Appl
26	47.4	0.4	2252	4	US-09-336-536-66 Sequence 66, Appl
27	47.2	0.4	1937	4	US-09-336-536-66 Sequence 66, Appl

C 28	47	0.4	2323	4	US-09-149-476-24 Sequence 24, Appl
C 29	46.4	0.4	144	1	US-08-702-344-26 Sequence 26, Appl
C 30	46.4	0.4	1098	3	US-09-248-335-35 Sequence 35, Appl
C 31	46.2	0.4	1023	1	US-08-252-966B-16 Sequence 16, Appl
C 32	46.2	0.4	2447	2	US-09-014-969-14 Sequence 14, Appl
C 33	46	0.4	578	4	US-09-602-877A-95 Sequence 27, Appl
C 34	46	0.4	1447	4	US-09-443-041A-27 Sequence 4, Appl
C 35	46	0.4	6755	3	US-08-931-999-4 Sequence 17, Appl
C 36	45.8	0.4	1307	2	US-08-960-022-17 Sequence 9, Appl
C 37	45.6	0.4	1172	1	US-07-945-288-9 Sequence 9, Appl
C 38	45.6	0.4	1172	1	US-08-462-831-9 Sequence 9, Appl
C 39	45.6	0.4	1172	1	US-08-461-809-9 Sequence 9, Appl
C 40	45.6	0.4	1172	1	US-08-461-441-9 Sequence 9, Appl
C 41	45.6	0.4	1172	5	PCT-US93-08518-9 Sequence 9, Appl
C 42	45.4	0.4	6004	4	US-08-961-527-27 Sequence 27, Appl
C 43	45.2	0.4	1445	4	US-09-814-951A-1 Sequence 1, Appl
C 44	45	0.4	2852	3	US-09-027-137-2 Sequence 2, Appl
C 45	45	0.4	2852	4	US-09-344-441-2 Sequence 2, Appl

ALIGNMENTS

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RESULT 1
US-09-388-917-1
: Sequence 1, Application US/09388917
: Patent No. 6258542
: GENERAL INFORMATION:
: APPLICANT: Hayashizaki, Yoshihide
: TITLE OF INVENTION: Method for Supporting DNA-Fixation and DNA-Fixed
: FILE REFERENCE: 1794-0120P
: CURRENT APPLICATION NUMBER: US/09/388, 917
: EARLIER FILING DATE: 1998-09-02
: EARLIER APPLICATION NUMBER: 10-250619
: EARLIER FILING DATE: 1998-09-04
: EARLIER APPLICATION NUMBER: 11-240910
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 1
: LENGTH: 222
: TYPE: DNA
: ORGANISM: Gallus gallus
US-09-388-917-1

Query Match      0.7%; Score 80.2; DB 4; Length 222;
Best Local Similarity 96.5%; Pred. No. 1.3e-11;
Matches 82; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 11861 GCAGTCCCGCTGTGTGACACACATGACATGAGTCTTGTAATCTTGTCCTTGG 11920
      |||||||
Db 1 GCAGTCCCGCTGTGTGACACACATGACATGAGTCTTGTAATCTTGTCCTTGG 60
      |||||||

QY 11921 CTTCTGCCCTGGCTGCTTAGG 11945
      |||||||
Db 61 CTTCTGCCCTGGCTGCTTAGG 85
      |||||||

RESULT 2
US-08-385-590A-3
: Sequence 3, Application US/08385590A
: Patent No. 5824861
: GENERAL INFORMATION:
: APPLICANT: Alwinckle, Herbert S.
: APPLICANT: No. 5824861e11, John I.
: TITLE OF INVENTION: TRANSGENIC POMACEOUS FRUIT WITH FIRE
: TITLE OF INVENTION: BRIGHT RESISTANCE
: NUMBER OF SEQUENCES: 28
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
: STREET: Clinton Square
: CITY: Rochester

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STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,590A
FILING DATE: 08-FEB-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,347
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/143
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 586 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-385-590A-3

Query Match 0.7%; Score 78.2; DB 1; Length 586;
Best Local Similarity 96.4%; Pred. No. 8,4e-11;
Matches 80; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 11863 ACTCCCGCTGTGTACGACACTGCAACATGAGCTTTGCTAATCTTGCTTGGCT 11922
Db 1 ACTCCCGCTGTGTACGACACTGCAACATGAGCTTTGCTAATCTTGCTTGGCTTGGCT 60
Qy 11923 TCCTGCCCTGCTGCTTGAAGG 11945
Db 61 TCCTGCCCTGCTGCTTGAAGG 83

RESULT 3
US-09-021-520-3
Sequence 3, Application US/09021520
Patent No. 6100453
GENERAL INFORMATION:
APPLICANT: Aldwinckle, Herbert S.
APPLICANT: No. 6100453e11, John L.
TITLE OF INVENTION: TRANSGENIC POMACEOUS FRUIT WITH FIRE
TITLE OF INVENTION: BLIGHT RESISTANCE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square
CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/021,520
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/385,590
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Goldman, Michael L.
REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/143
TELEPHONE: (716) 263-1304
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 586 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-09-021-520-3

Query Match 0.7%; Score 78.2; DB 3; Length 586;
Best Local Similarity 96.4%; Pred. No. 8,4e-11;
Matches 80; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 11863 ACTCCCGCTGTGTACGACACTGCAACATGAGCTTTGCTAATCTTGCTTGGCT 11922
Db 1 ACTCCCGCTGTGTACGACACTGCAACATGAGCTTTGCTAATCTTGCTTGGCTTGGCT 60
Qy 11923 TCCTGCCCTGCTGCTTGAAGG 11945
Db 61 TCCTGCCCTGCTGCTTGAAGG 83

RESULT 4
US-08-232-463-14
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single


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; TOPLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: PTZgpt-F13
US-08-232-463-14

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Query Match 0.58; Score 62.6; DB 1; Length 7218;
Best Local Similarity 5.68; Pred. No. 6.8e-06;
Matches 23; Conservative 227; Mismatches 161; Indels 0; Gaps 0;

OY	7540	GGGGGCTCATATGCGTTCAGCTCCTGCTCGTTGCACGACCAAAATTTCAGATCACCC	7599
Db	1055	GGACTTGCCATYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY	11144
OY	7600	AGTTGTCTCATCACTTCCTGTCCTCATCTTCCAGCTGTATCTTGACAAT	7659
Db	1115	YY	11747
OY	7660	ACAGGCTATTTTGTGTTGCTTCAGACGCCATTAAATTCTTCAGTGCATCTGTCT	7719
Db	1175	YY	12343
OY	7720	GTTGATGCCACCTGGAACAGSATTTCAGCAGCTTGCAAAGAACAATCAGTCGAACCT	7779
Db	1235	YY	12944
OY	7780	TCTGCATTCATAATTCTTACCAGTCTCTCTGTGTGAGTAGGCCAATAATTACTAGAA	7839
Db	1295	YY	13544
OY	7840	C TTTCGTCAC TGACA AGTTATG CATT TTA TTA CTCT ATTA TGA GTA CTT GA CAT AA	7899
Db	1355	YY	14144
OY	7900	CACAGACGCCACATATTTTGGCGGGATTTCCACAGTGTCTCTGTGCTCT	7950
Db	1415	YYYYYYYYYYYYYYYYYGNACCAAAATCTGCATCTCTTAATCACTCTT	1465

RESULT 5
 US-07-999-280A-23
 : Sequence 23, Application US/07999280A
 : Patent No. 3573950
 : GENERAL INFORMATION:
 : APPLICANT: LADNER, MARTHA B.
 : APPLICANT: NOBLE, JANELLE A.
 : APPLICANT: MARTIN, GEORGE A.
 : APPLICANT: KAWASKI, ERNEST S.
 : APPLICANT: COYNE, MAZIE YEE
 : APPLICANT: HALENBECK, ROBERT F.
 : APPLICANT: KOTHS, KIRSTON E.
 : TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
 : NUMBER OF SEQUENCES: 24
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: CHIRON CORPORATION
 : STREET: Intellectual Property - R440, P.O. Box 8097
 : CITY: Emeryville
 : STATE: California
 : COUNTRY: U.S.A.
 : ZIP: 94662-8097
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/07/999,280A
 : FILING DATE: 28-DEC-1992
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: McGarrigle Jr., Philip L.
 : REGISTRATION NUMBER: 31,395
 : REFERENCE/DOCKET NUMBER: 0681.007
 : TELECOMMUNICATION INFORMATION:

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1 TELEPHONE: (510) 601-2718
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3 TELEFAX: (510) 655-3542
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Query Match	0.58;	Score 56.4;	DB 1;	Length 1987;
Best Local Similarity	59.38;	Pred. No. 0.00013;		
Matches 96;	Conservative 0;	Mismatches 66;	Indels 0;	Gaps 0;

QY	11037	TCCACATCTTCCCTGACTGGGGGGCCCCAGGCCTGAATGACGTACTCAGATTGGGGCTTC	11098
Db	1772	TCATGTGCCCTTGAAAATGTTGGCGCCCACGCCCTGGACACAGTACTCCAATGTTGTCTG	1831
QY	11097	AAAGAGCACAGTAAGAAGAGGAGCAATCACTCTCCACCCTGCTGGGCAAGCCTCTTCTG	11156
Db	1832	ACAAGCTCAAGATACAGTGGGACGGTGTCTCTCTTGATCTGGACAGTACTCTTCTCATTC	1891
QY	11157	ATGAGAGCCCTTGATCAACTGGCTCTTGAGATGCAACTTCT	11198
Db	1892	GTCGAGATTAGATCACATTAGTTTAAACAGCTGCATATAT	1933

RESULT 6
US-08-426-036-23
: Sequence 23, Application US/08426036
Patent No. 5643563
GENERAL INFORMATION:
APPLICANT: LADNER, MARTHA B.
APPLICANT: NOBLE, JANELLE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: HALENECK, ROBERT F.
APPLICANT: KOTHS, KRISTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHITON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,036
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle Jr., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681.014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
TELEX: n/a

```

? INFORMATION FOR SEQ ID NO: 23:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1987 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 70..1726
? FEATURE:
? NAME/KEY: mat-peptide
? LOCATION: 166..1726
? US-08-426-036-23

Query Match 0.58; Score 56.4; DB 1; Length 1987;
Best Local Similarity 59.38; Pred. No. 0.00013;
Matches 96; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 11037 TCCACATCTTCCTGCTAGTGGGGGCCCGAGGCTCAATGACAGTACTCCAGATGGGGCCNC 11096
Db 1772 TCAATGTCCCTCTGCAAAATGTGGCCGCCAGCCCTGACACATCTCCAGATGTTGCTG 1831
Qy 11097 AAAAGAGCAGAGTAAGAAGGAGACATCACTTCTCTCACCTGCTGGCCAGGCTCTCTG 1156
Db 1832 ACCAGCTCAGAGTACAGTGGGACGGTGTCTGCTTGTATCTGGACAGTACTTCTTACTC 1891
Qy 11157 ATGAGGCCCTGGATNCAACTGGCTTCTGAGCTGCACTTCT 11198
Db 1892 GTGCAGATTAAAGATCACAATTAGTTTAAACAGCTGCATCATAT 1933

RESULT 7
US-08-426-279-23
? Sequence 23, Application US/08426279
? Patent No. 5672343
? GENERAL INFORMATION:
? APPLICANT: LADNER, MARTHA B.
? APPLICANT: NOBLE, JANELLE A.
? APPLICANT: MARTIN, GEORGE A.
? APPLICANT: KAWASAKI, ERNEST S.
? APPLICANT: COYNE, MAZIE YEE
? APPLICANT: HALENBECK, ROBERT F.
? APPLICANT: KOHS, KIRSTON E.
? TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
? NUMBER OF SEQUENCES: 24
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: CHIRON CORPORATION
? STREET: Intellectual Property - R440, P.O. Box 8097
? City: Emeryville
? STATE: California
? COUNTRY: U.S.A.
? ZIP: 94662-8097
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/426,279
? FILING DATE: 21-APR-1995
? CLASSIFICATION: 530
? ATTORNEY/AGENT INFORMATION:
? NAME: McGarrigle Jr., Philip L.
? REGISTRATION NUMBER: 31,395
? REFERENCE/DOCKET NUMBER: 0681.013
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (510) 601-2718
? TELEFAX: (510) 655-3542
? TELEX: n/a
? INFORMATION FOR SEQ ID NO: 23:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1987 base pairs

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1 TYPE: nucleic acid
2 STRANDEDNESS: single
3 TOPOLOGY: linear
4 MOLECULE TYPE: DNA (genomic)
5 FEATURE:
6 NAME/KEY: CDS
7 LOCATION: 70..1726
8 NAME/KEY: mat_peptide
9 LOCATION: 166..1726
10 US-08-426-279-23
11
12 Query Match 0.5%; Score 56.4; DB 1; Length 1987;
13 Match Local Similarity 59.3%; Pred. No. 0.00013;
14 Matches 96; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
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16 Oy 11037 TCACATCTTTCCTGTACTGAGGGGCCCCAGGCGCTTAATGACATCTCCAGATGGGGCCTC 11096
17 Db 1772 TCAGTGTCCCTGTGAATAATGTGGGCCCCAGGCGCTTGACACATCTCCAGATGTGTCTG 1831
18 Oy 11097 AAAGAGCAGACACTAAGAAGGAGCAATCACTTCTCACCCTGCTGGCCACCCCTTTCTG 11156
19 Db 1832 ACCACCTCAGAGTACAGCGGAGCGGCTGTCTTCTTGATCTGGACAGTACTTCTACTC 1891
20 Oy 11157 ATGGAGCCCTGGATCACTGCGCTTCTGAGCTGCACTTCT 11198
21 Db 1892 GTCCAGATTAAAGATCACAATTACTTTTAAACAGCTGCATCATAT 1933
22
23 RESULT 8
24 US-08-401-013-23
25 Sequence 23, Application US/08401013
26 Patent No. 5681719
27 GENERAL INFORMATION:
28 APPLICANT: LADNER, MARTHA B.
29 APPLICANT: NOBLE, JANELLE A.
30 APPLICANT: MARTIN, GEORGE A.
31 APPLICANT: KAMASAKI, ERNEST S.
32 APPLICANT: COYNE, MAZIE YEE
33 APPLICANT: HALENBECK, ROBERT F.
34 APPLICANT: KOTHS, KIRSTON E.
35 TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
36 NUMBER OF SEQUENCES: 24
37 CORRESPONDENCE ADDRESS:
38 ADDRESSEE: CHIRON CORPORATION
39 STREET: Intellectual Property - R440, P.O. Box 8097
40 CITY: Emeryville
41 STATE: California
42 COUNTRY: U.S.A.
43 ZIP: 94662-8097
44 COMPUTER READABLE FORM:
45 MEDIUM TYPE: floppy disk
46 COMPUTER: IBM PC compatible
47 OPERATING SYSTEM: PC-DOS/MS-DOS
48 SOFTWARE: PatentIn Release #1.0, Version #1.25
49 CURRENT APPLICATION DATA:
50 APPLICATION NUMBER: US/08/401.013
51 FILING DATE: 08-MAR-1995
52 CLASSIFICATION: 435
53 PRIOR APPLICATION DATA:
54 APPLICATION NUMBER: US 07/999,280
55 FILING DATE: 28-DEC-1992
56 ATTORNEY/AGENT INFORMATION:
57 NAME: Mcgarigle Jr., Philip L.
58 REGISTRATION NUMBER: 31,395
59 REFERENCE/DOCKET NUMBER: 0681,007
60 TELECOMMUNICATION INFORMATION:
61 TELEPHONE: (510) 601-2718
62 TELEFAX: (510) 655-3542
63 TELEX: N/A
64 INFORMATION FOR SEQ ID NO: 23:
65 SEQUENCE CHARACTERISTICS:
66 LENGTH: 1987 base pairs

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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 70..1726
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 166..1726
US-08-401-013-23

Query Match
Best Local Similarity 59.3%; Score 56.4; DB 1; Length 1987;
Pred. No. 0.00013;
Matches 96; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 11037 TCACATCTTCTCTGACTGGGGGCCCCGAGCCCTGATGACAGTCTCCAGATGGGGCCTC 11096
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QY 11157 ATGAGACCCCTGGATACACTGGCTTCTGAGCTGCACTTCT 11198
DB 1892 GTGCAGATTAAAGTACATTAGTTTAAACAGCTGCATCATAT 1933

RESULT 9

US-08-426-570-23
Sequence 23, Application US/08426570
Patent No. 6103224
GENERAL INFORMATION:
APPLICANT: LADNER, MARTHA B.
APPLICANT: NOBLE, JANELLE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: HALENECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 21-APR-1995
APPLICATION NUMBER: US/08/426,570
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle Jr., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681,012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
TELEX: n/a
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1987 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 70..1726
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 166..1726
US-08-426-570-23

Query Match
Best Local Similarity 59.3%; Score 56.4; DB 3; Length 1987;
Pred. No. 0.00013;
Matches 96; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

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RESULT 10

US-08-425-876-23
Sequence 23, Application US/08425876
Patent No. 6117422
GENERAL INFORMATION:
APPLICANT: LADNER, MARTHA B.
APPLICANT: NOBLE, JANELLE A.
APPLICANT: MARTIN, GEORGE A.
APPLICANT: KAWASAKI, ERNEST S.
APPLICANT: COYNE, MAZIE YEE
APPLICANT: HALENECK, ROBERT F.
APPLICANT: KOTHS, KIRSTON E.
TITLE OF INVENTION: NEW FORMS OF COLONY STIMULATING FACTOR-1
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 21-APR-1995
APPLICATION NUMBER: US/08/425,876
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McGarrigle Jr., Philip L.
REGISTRATION NUMBER: 31,395
REFERENCE/DOCKET NUMBER: 0681,011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2718
TELEFAX: (510) 655-3542
TELEX: n/a
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 1987 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS

GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 27, 2003, 03:57:23 ; Search time 22135 Seconds

(without alignments)
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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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ALIGNMENTS

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LOCUS Gallus gallus lysozyme precursor, gene, partial cds.
DEFINITION AF405540
ACCESSION AF405540
VERSION AF405540.1 GI:15487991
KEYWORDS
SOURCE Gallus gallus.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus
REFERENCE
1 (bases 1 to 11945)
Rapp,J.C.
TITLE Chicken Lysozyme Promoter

JOURNAL REFERENCE AUTHORS TITLE	JOURNAL SUBMITTED	GEORGIA	LOCATION/QUALIFIERS	FEATURES SOURCE	misc_feature	mRNA	CDS	s1g-peptide	BASE COUNT	ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;			
Matches 11945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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QY	421	TATGGAAGACGTGATCGGAACTTGAGGTTTTTATTTAATAGTGTGGCTTGAAGCTTGA	480
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Dh 3841 AGAGAGCTAACTCTATGCTATGCTGAAGGTAAAGTGGTTTTAAAAAGAAACACAA 3900
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Dh 3901 AGGCAAAACCGGCTGCCCATGAGAAAGCAGTGTGAATATGTTAGAAAGTGCAG 3960

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Db 3961 AAGCCCCAGGAGTGTGACAGGCCCTCTGCCACTAGAGCGGGAACAAGCTTCCCT 4020
OY 4021 GCGTAGGGCTGTGGCCGGAGAGTGGTCTTCTTGGTGGTCTTGTGGCGTTGGCT 4080
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Db 4021 GCGTAGGGCTGTGGCCGGAGAGTGGTCTTCTTGGTGGTCTTGTGGCGTTGGCT 4080
OY 4081 TTGAGATTTAGACACAAGGGAAGCCTGAAGAGAGTGTGGGCACTATTTTGGTTGTA 4140
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Db 4081 TTGAGATTTAGACACAAGGGAAGCCTGAAGAGAGTGTGGGCACTATTTTGGTTGTA 4140
OY 4141 AGCCTGACTCTCAAAATATATTTTGTGAGGAGTGTAGCAATTTGCCAATTTAAATA 4200
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Db 4141 AGCCTGACTCTCAAAATATATTTTGTGAGGAGTGTAGCAATTTGCCAATTTAAATA 4200
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Db 4261 GAACTACTGCTCTTAAACACTTGTGTGAGTGTGAGACCTTGGATAGTGTGCTCTT 4320
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Db 4321 GTTACATGTGTGATGACATCTTGTCTTTCATCCACATCCATGCTTCCATCCCA 4380
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Db 5161 CACTGATGAGAGTAGTAAATAAGAGACGATTCAGACACCAACGAGAGTGTGGCG 5220
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D 6721 ACAGCTTCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 6780
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Qy	10561	ACTTATATCAATCATAGATCATAGATGAGCTGGGTTGGAAGGGACCCCAAGATCATG	10620
Dh	10561	ACTTATATCAATCATAGATCATAGATGAGCTGGGTTGGAAGGGACCCCAAGATCATG	10620
Qy	10621	AAGATCCAAACACCCCGCCACAGGAGGGCCACCACTCCAGATCTGTGTAAGCCAG	10680
Dh	10621	AAGATCCAAACACCCCGCCACAGGAGGGCCACCACTCCAGATCTGTGTAAGCCAG	10680
Qy	10681	GCAGCCGAGGGCTCCATCAACCTGGCCATGAAACCTCCAGGGATGGAAGATCCACAAAC	10740
Dh	10681	GCAGCCGAGGGCTCCATCAACCTGGCCATGAAACCTCCAGGGATGGAAGATCCACAAAC	10740
Qy	10741	CTCTGTGGGACGCCGTGTGCCACGACACCTCCTGTGTGAAGAACTTTTCCCTGAC	10800
Dh	10741	CTCTGTGGGACGCCGTGTGCCACGACACCTCCTGTGTGAAGAACTTTTCCCTGAC	10800
Qy	10801	ATCCAAATCTAAGCCTTCCCTCCTTAGAGTTAGATCCACTCCCCCTTGTGTACTACTGTG	10860
Dh	10801	ATCCAAATCTAAGCCTTCCCTCCTTAGAGTTAGATCCACTCCCCCTTGTGTACTACTGTG	10860
Qy	10861	TACTCTGTGAAAAAATTTGATTTCTCCCTCTTTTGGAAAGTTGACATGAGGTCCTTGCA	10920
Dh	10861	TACTCTGTGAAAAAATTTGATTTCTCCCTCTTTTGGAAAGTTGACATGAGGTCCTTGCA	10920
Qy	10921	GCCCTTCTTCTCTTCGACAGATGAACAAGCCGAGCTCCCTCAGCCTGTCTTTATAGAGA	10980
Dh	10921	GCCCTTCTTCTCTTCGACAGATGAACAAGCCGAGCTCCCTCAGCCTGTCTTTATAGAGA	10980
Qy	10981	GGTGCTCCAGCCCTCTGATCATCTTTGTGTGGCCTCTCTGGAACCGGCTCCAAAGCTCA	11040
Dh	10981	GGTGCTCCAGCCCTCTGATCATCTTTGTGTGGCCTCTCTGGAACCGGCTCCAAAGCTCA	11040
Qy	11041	CATCTTCTCCTGACTGGGGGCCCCAGGCGCTGAATCAGACTCCAGATGGGGCTCAAAA	11100
Dh	11041	CATCTTCTCCTGACTGGGGGCCCCAGGCGCTGAATCAGACTCCAGATGGGGCTCAAAA	11100
Qy	11101	GAGCAGAGTAAGAAGGGAGACATCACCTTCTCACCTGTGTGGGACCCCTCTTGATGG	11160
Dh	11101	GAGCAGAGTAAGAAGGGAGACATCACCTTCTCACCTGTGTGGGACCCCTCTTGATGG	11160
Qy	11161	AGCCCTGGATTACAATGGCTTTCTAGCTGCAAACTTCTCTTATAGATTCCACTTTAAA	11220
Dh	11161	AGCCCTGGATTACAATGGCTTTCTAGCTGCAAACTTCTCTTATAGATTCCACTTTAAA	11220
Qy	11221	ACAGGACAATTCACAAGGTGTGTAGGGCAGTAGAGAGTTTTCACACTTCTCATTTTC	11280
Dh	11221	ACAGGACAATTCACAAGGTGTGTAGGGCAGTAGAGAGTTTTCACACTTCTCATTTTC	11280
Qy	11281	GCTAGATCTTTAGATGANGAAGCTGTGAAGTTGTGCTTGTGCGTGTCTTCTCCCTCAA	11340
Dh	11281	GCTAGATCTTTAGATGANGAAGCTGTGAAGTTGTGCTTGTGCGTGTCTTCTCCCTCAA	11340
Qy	11341	ATATCTCTGTGCTGATTAACCTCACCCCACTGCCACTGATGGCTCCATGGCCCCCTGCAGC	11400
Dh	11341	ATATCTCTGTGCTGATTAACCTCACCCCACTGCCACTGATGGCTCCATGGCCCCCTGCAGC	11400
Qy	11401	CAGGGCCCGTGAAGAACCCGGGACCTGCTCAGATGTGCGTTTATFACACAGTGTGACCAAG	11460
Dh	11401	CAGGGCCCGTGAAGAACCCGGGACCTGCTCAGATGTGCGTTTATFACACAGTGTGACCAAG	11460
Qy	11461	TTGCACCTTATGATACACAAACAAATGTGTGGATCTCTTCAGCACTTGAAGAAAGAGCA	11520
Dh	11461	TTGCACCTTATGATACACAAACAAATGTGTGGATCTCTTCAGCACTTGAAGAAAGAGCA	11520
Qy	11521	AATTTGCATTTGCAGGAAATGTTTAGTAATTTCTGCCAATTTAAACTTGTATTATACCA	11580
Dh	11521	AATTTGCATTTGCAGGAAATGTTTAGTAATTTCTGCCAATTTAAACTTGTATTATACCA	11580
Qy	11581	TGGGTGTTTTTATGTGCTGTATAGTGTGACCTGATATGAAACAATGGCTATGCAAGTAA	11640
Dh	11581	TGGGTGTTTTTATGTGCTGTATAGTGTGACCTGATATGAAACAATGGCTATGCAAGTAA	11640

QY	11641	AAAAGCGCTGACGATATTTGCAACAGACTATAAAATTCCTGTGCGCTTGAGCCAAATGTGG	11700
DB	11641	AATCAGACTCTGATGATTTGCAACAGACTATAAAATTCCTGTGCGCTTGAGCCAAATGTGG	11700
QY	11701	TACTTCCCAACATTTGATTAAGAAATTTTGCAAGTTTACAGCAATGTTTGAAGTGTGTGGAA	11760
DB	11701	TACTTCCCAACATTTGATTAAGAAATTTTGCAAGTTTACAGCAATGTTTGAAGTGTGTGGAA	11760
QY	11761	ATTTCTGTATCTCAGAGGCGCTTTTGGACACTGTAGAAACAGAGCAATCAAAAGGGG	11820
DB	11761	ATTTCTGTATCTCAGAGGCGCTTTTGGACACTGTAGAAACAGAGCAATCAAAAGGGG	11820
QY	11821	TGGGAGGAAGTTAAAGAGAGGCGAGGCAAGAGACTTGCAATCCCGCTGTGTACG	11880
DB	11821	TGGGAGGAAGTTAAAGAGAGGCGAGGCAAGAGACTTGCAATCCCGCTGTGTACG	11880
QY	11881	ACACTGGCAACATGAGTCTTTGGCTAATCTTGCTGTGCTTCCCTCCCTGGCTGCT	11940
DB	11881	ACACTGGCAACATGAGTCTTTGGCTAATCTTGCTGTGCTTCCCTCCCTGGCTGCT	11940
QY	11941	TAGGG 11945	
DB	11941	TAGGG 11945	
RESULT 2			
AF405538			
LOCUS	AF405538	12728 bp	DNA linear SYN 06-SEP-2001
DEFINITION	Synthetic construct lysozyme signal peptide/modified human interferon alpha 2b fusion protein precursor, gene, complete cds.		
ACCESSION	AF405538		
VERSION	AF405538.1	GI:15487987	
KEYWORDS			
SOURCE	synthetic construct.		
ORGANISM	synthetic construct		
REFERENCE	1 (bases 1 to 12728)		
AUTHORS	Rapp, J.C.		
TITLE	Chicken lysozyme Promoter		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 12728)		
AUTHORS	Rapp, J.C.		
TITLE	Direct Submission		
JOURNAL	Submitted (06-AUG-2001) Avigenics Inc, 425 River Road, Athens, Georgia 30602-2771, USA		
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	/note="cloning vector pAVICR-A115.93.1.2"		
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	/note="derived from chicken lysozyme"		
BASE COUNT	3337 a 2755 c 2850 g 3786 t		
ORIGIN			
Query Match	100.0%; Score 11945; DB 12; Length 12728;		
Best Local Similarity	100.0%; Pred. No. 0;		
Matches 11945; Conservative	0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	TCGCGCTTCTTGAATTCACCTGTTGTAATTCATCTCTTGGCCGATGAAGATA 60	

[illegible]

QY	1141	AGCGCATGGTTTAAACACAGTTGACAGATGCTAACAGAGTACACGCTTTATGCGAAG	1200
Db	1141	AGTGCATAGTTTTAAACACAGTTGACAGATGCTAACAGAGTACACGCTTTATGCGAAG	1200
QY	1201	TGATGCCGATGAGCTGCTTGTGACGCTGTTTACGGCAGCTGCTTGACAGTATTCAGAT	1260
Db	1201	TGATGCCGATGAGCTGCTTGTGACGCTGTTTACGGCAGCTGCTTGACAGTATTCAGAT	1260
QY	1261	AGGGGTGGGGTGTCTTTGTGTCGTCTTCCACACGCTGCCACACAGCCACTCCCGAACA	1320
Db	1261	AGGGGTGGGGTGTCTTTGTGTCGTCTTCCACACGCTGCCACACAGCCACTCCCGAACA	1320
QY	1321	CATCTCACCTCTGGGTACTTTTCAACACATCTTACAGAGTAGATGATGTTACTATGAA	1380
Db	1321	CATCTCACCTCTGGGTACTTTTCAACACATCTTACAGAGTAGATGATGTTACTATGAA	1380
QY	1381	ACAGAGAAGTCTCTCAGTTGGATATTCATCAGGAGATGCTTTTTTCCATGTTGGGCAAA	1440
Db	1381	ACAGAGAAGTCTCTCAGTTGGATATTCATCAGGAGATGCTTTTTTCCATGTTGGGCAAA	1440
QY	1441	GTATGATTAACCATCTCTATTTTGTAAATTATGACATTGTAGTCCGTGAATCCTTTCAT	1500
Db	1441	GTATGATTAACCATCTCTATTTTGTAAATTATGACATTGTAGTCCGTGAATCCTTTCAT	1500
QY	1501	AGCACACCTTATTTGACACAGGTGTAGGCTGTGCTGTGGCCTGTGCTGTGCTTCAATCTT	1560
Db	1501	AGCACACCTTATTTGACACAGGTGTAGGCTGTGCTGTGGCCTGTGCTGTGCTTCAATCTT	1560
QY	1561	TTTAAGGCTCTTTGGAAATACCTGACTGTGATTTGAAGTCTCTTGAAGATAGTAAACAGTA	1620
Db	1561	TTTAAGGCTCTTTGGAAATACCTGACTGTGATTTGAAGTCTCTTGAAGATAGTAAACAGTA	1620
QY	1621	CTTACCTTTGATCCCAATGGAATCGAGCATCTTCACTGTTGTAAAGAATTCGCCCTATTCAT	1680
Db	1621	CTTACCTTTGATCCCAATGGAATCGAGCATCTTCACTGTTGTAAAGAATTCGCCCTATTCAT	1680
QY	1681	ACCATGTAATGTAAATTTTAAACCCCGACGTGCTGACACTTTGGATATATTCAGATATAG	1740
Db	1681	ACCATGTAATGTAAATTTTAAACCCCGACGTGCTGACACTTTGGATATATTCAGATATAG	1740
QY	1741	ACCTTGGCCCTACCCCTCTTGTGTACTGATATTTGTATAGAAATATTTTAAACGTGCA	1800
Db	1741	ACCTTGGCCCTACCCCTCTTGTGTACTGATATTTGTATAGAAATATTTTAAACGTGCA	1800
QY	1801	TATGATTAATTAACATTATGAAAGAGACATCTGCTGATCTTCAAAATGTAAAGAAATGAGAGA	1860
Db	1801	TATGATTAATTAACATTATGAAAGAGACATCTGCTGATCTTCAAAATGTAAAGAAATGAGAGA	1860
QY	1861	GTGGGTGTGCTTTATTAATATACAAGATTTGCAAAATTAATGCAAGGTGCTTAAAAAAA	1920
Db	1861	GTGGGTGTGCTTTATTAATATACAAGATTTGCAAAATTAATGCAAGGTGCTTAAAAAAA	1920
QY	1921	AAAAAAAAGCTAATATATATAAAGACCAAGTGTTTTCAAGTGAATATACATTCCTATTTGG	1980
Db	1921	AAAAAAAAGCTAATATATATAAAGACCAAGTGTTTTCAAGTGAATATACATTCCTATTTGG	1980
QY	1981	TAAACAGCTTACATTTTATATGAAATATACCAAGCGCTGCTACCTTTCAAAACATAAAGCTGT	2040
Db	1981	TAAACAGCTTACATTTTATATGAAATATACCAAGCGCTGCTACCTTTCAAAACATAAAGCTGT	2040
QY	2041	ATTGTCTCTCGTACCATTTGCAATTTCTCATTTCCCAATTTGACAAAGATGTCTGGGTAA	2100
Db	2041	ATTGTCTCTCGTACCATTTGCAATTTCTCATTTCCCAATTTGACAAAGATGTCTGGGTAA	2100
QY	2101	ACTATTTCAAGAAATGGCTTTGGAATACACAGATGGAGCTTGTCTAGTTGGATATGACAG	2160
Db	2101	ACTATTTCAAGAAATGGCTTTGGAATACACAGATGGAGCTTGTCTAGTTGGATATGACAG	2160
QY	2161	TTTGACACTGCAAAATGTACAGAAATGATGTCTCTAGATGCCCCAATCTCAAAGATTTT	2220
Db	2161	TTTGACACTGCAAAATGTACAGAAATGATGTCTCTAGATGCCCCAATCTCAAAGATTTT	2220

[illegible]

Db	3301	CAGGGAAAAGTGGGTAACTATTTTAACTAGTGTGGCAAAAGCTCATCTGCAAT	3360
QY	3361	ACGTAGGGTGTACTCTCCGAAGTTAAACAGTGTGGGTCAGTAATATATGGATGAATTC	3420
Db	3361	ACGTAGGGTGTGTACTCTCCGAAGTTAAACAGTGTGGGTCAGTAATATATGGATGAATTC	3420
QY	3421	ACAGTGAAGCATTTCAAGGGTAGATCATCTAACGACACGATCATCAAGCTATGATTTGG	3480
Db	3421	ACAGTGAAGCATTTCAAGGGTAGATCATCTAACGACACGATCATCAAGCTATGATTTGG	3480
QY	3481	AAGCGGTATCGAAGAGCAGAGAAAGTAGCACTTTCATATGTTTTCCCTCCACGTAAA	3540
Db	3481	AAGCGGTATCGAAGAGCAGAGAAAGTAGCACTTTCATATGTTTTCCCTCCACGTAAA	3540
QY	3541	GCAGCTGTGGAAAGTACACCCCTTGAGCAGACAGAAATTAATTCAGAGGCAATGTGC	3600
Db	3541	GCAGCTGTGGAAAGTACACCCCTTGAGCAGACAGAAATTAATTCAGAGGCAATGTGC	3600
QY	3601	TAGGAACATTTCTTGCTGAATTCATCTTACCTTCAGACATTTGATGGCTGGCTTGTGGTCC	3660
Db	3601	TAGGAACATTTCTTGCTGAATTCATCTTACCTTCAGACATTTGATGGCTGGCTTGTGGTCC	3660
QY	3661	TTTCTCAGCACCCTCAGAGGCCAGAGCCTTGTGTAGCTGTGAGGAAAGATTCTGTCAA	3720
Db	3661	TTTCTCAGCACCCTCAGAGGCCAGAGCCTTGTGTAGCTGTGAGGAAAGATTCTGTCAA	3720
QY	3721	GTCCAAAGTTTAGAGAGTCATATGCTTTGGTTTCCCCACACGTGACAGCAAGATGG	3780
Db	3721	GTCCAAAGTTTAGAGAGTCATATGCTTTGGTTTCCCCACACGTGACAGCAAGATGG	3780
QY	3781	AACGTATGTCGAAGCCTCTGTCCACTACCTGTTGCTGCAGAGCAGACTGCTCCAGAAA	3840
Db	3781	AACGTATGTCGAAGCCTCTGTCCACTACCTGTTGCTGCAGAGCAGACTGCTCCAGAAA	3840
QY	3841	AGAGAGCTAACTATATGCCATAGTCTGAAAGTAAATGGGTTTTTAAAAAGAAAACACAA	3900
Db	3841	AGAGAGCTAACTATATGCCATAGTCTGAAAGTAAATGGGTTTTTAAAAAGAAAACACAA	3900
QY	3901	AGGCAAAACGGGCGCCCATGAAAGAAAGCAGTGTAAACATGGTGAAGAAAGGTGCAG	3960
Db	3901	AGGCAAAACGGGCGCCCATGAAAGAAAGCAGTGTAAACATGGTGAAGAAAGGTGCAG	3960
QY	3961	AAGCCCCAGGCACTGTGACAGGCCCTCTGCACACTAGAGGCGGGAAACAAGCTCCCT	4020
Db	3961	AAGCCCCAGGCACTGTGACAGGCCCTCTGCACACTAGAGGCGGGAAACAAGCTCCCT	4020
QY	4021	GCCTAGGGCTGTGCCCGCAGAGTGCCTTTCTTGGTGGGTTTTGTTGGCGTTGGTT	4080
Db	4021	GCCTAGGGCTGTGCCCGCAGAGTGCCTTTCTTGGTGGGTTTTGTTGGCGTTGGTT	4080
QY	4081	TTTGAGATTTAAACACAAGGGAGGCTGTAAAGGAGGTTGGGCACTATTTTGGTTGTA	4140
Db	4081	TTTGAGATTTAAACACAAGGGAGGCTGTAAAGGAGGTTGGGCACTATTTTGGTTGTA	4140
QY	4141	AAGCGTACTTCAATATATATTTTGTGAGAGAGTGTACGAAATTTGGCAATTTAAATA	4200
Db	4141	AAGCGTACTTCAATATATATTTTGTGAGAGAGTGTACGAAATTTGGCAATTTAAATA	4200
QY	4201	AAGTTGCAAGAGATTGAAGCGTAGTAGTGAGAGGGTAACAGTTTAAAGATCTTCT	4260
Db	4201	AAGTTGCAAGAGATTGAAGCGTAGTAGTGAGAGGGTAACAGTTTAAAGATCTTCT	4260
QY	4261	CAAACTACTGCTTTAAACACTTGTGTGAGTGTGAGACCTTGGATAGGTAGAGTCTTT	4320
Db	4261	CAAACTACTGCTTTAAACACTTGTGTGAGTGTGAGACCTTGGATAGGTAGAGTCTTT	4320
QY	4321	GTATACATGTCGATGACACTTGTGTGCTTTTCCATATCCACATATCCATGATTCACATCA	4380
Db	4321	GTATACATGTCGATGACACTTGTGTGCTTTTCCATATCCACATATCCATGATTCACATCA	4380
QY	4381	CGCATTTGTCAATATCCATATCTGTCAATATGCAATACACTGCTCTTGTGACTATGG	4440

Db	4381	CGCATTTGCACTTATCCCATATCTGTCAATCTGACATACCTGTCTCTCTGCACTTGG	4440
Qy	4441	TCAGAGAAGAGATGTATTAATCCCAAGCCGCCAAGTTTGAGAAGATGGCACTTGGT	4500
Db	4441	TCAGAGAAGAGATGTATTAATCCCAAGCCGCCAAGTTTGAGAAGATGGCACTTGGT	4500
Qy	4501	TCCTTCCCTTTTCTGCTAGTAAAGATTTTCTCTGGCTTTGACACTCAGCAATAG	4560
Db	4501	TCCTTCCCTTTTCTGCTAGTAAAGATTTTCTCTGGCTTTGACACTCAGCAATAG	4560
Qy	4561	TCCTTCCCTTTTCTGCTAGTAAAGATTTTCTCTGGCTTTGACACTCAGCAATAG	4620
Db	4561	TCCTTCCCTTTTCTGCTAGTAAAGATTTTCTCTGGCTTTGACACTCAGCAATAG	4620
Qy	4621	TTTGTGTCTTCTCTACTCTTAAAGTAAAGTCTTAAAGTAAAGTAAAGTAAAGT	4680
Db	4621	TTTGTGTCTTCTCTACTCTTAAAGTAAAGTCTTAAAGTAAAGTAAAGTAAAGT	4680
Qy	4681	GTGGCCGAGTCTCTGATGAACACACCTGATATGGCCAAAGTGGGTGGTTC	4740
Db	4681	GTGGCCGAGTCTCTGATGAACACACCTGATATGGCCAAAGTGGGTGGTTC	4740
Qy	4741	TCGAGGAACGGGAGGCTTTTGGCTCTGAAAGCAAGAGCTCTGGGAGTTGCACTTAT	4800
Db	4741	TCGAGGAACGGGAGGCTTTTGGCTCTGAAAGCAAGAGCTCTGGGAGTTGCACTTAT	4800
Qy	4801	TTGCAACTGATGTGGGAAGTGTGCTTAAAGCAGATTCCTAGTTCCTGCTACTTCT	4860
Db	4801	TTGCAACTGATGTGGGAAGTGTGCTTAAAGCAGATTCCTAGTTCCTGCTACTTCT	4860
Qy	4861	TTTCTTCTTGGCAGTCACTTATTTCTGACAGACAAACAGCCACCTGACAGCTTA	4920
Db	4861	TTTCTTCTTGGCAGTCACTTATTTCTGACAGACAAACAGCCACCTGACAGCTTA	4920
Qy	4921	GAAAGTATGTGGCTGTGCTGGGTGTGTTACAGCTCTGCCCTGTGAAAGGGATTTAAA	4980
Db	4921	GAAAGTATGTGGCTGTGCTGGGTGTGTTACAGCTCTGCCCTGTGAAAGGGATTTAAA	4980
Qy	4981	CGGGACCACTTATCCCAAGAGATCTCATTCATGATGAAGTGAAGTGAAGTGAAGT	5040
Db	4981	CGGGACCACTTATCCCAAGAGATCTCATTCATGATGAAGTGAAGTGAAGTGAAGT	5040
Qy	5041	CTCCAACTTCAAAACATTAATTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGT	5100
Db	5041	CTCCAACTTCAAAACATTAATTTGAGTGAAGTGAAGTGAAGTGAAGTGAAGT	5100
Qy	5101	TAAATCATTTAGTGTGAGCTCTGACAGCATGTAGTGTGGCAGCTCCCACTTCTCAAGAC	5160
Db	5101	TAAATCATTTAGTGTGAGCTCTGACAGCATGTAGTGTGGCAGCTCCCACTTCTCAAGAC	5160
Qy	5161	CAGTATGAGAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT	5220
Db	5161	CAGTATGAGAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT	5220
Qy	5221	AAGAAATGATGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT	5280
Db	5221	AAGAAATGATGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT	5280
Qy	5281	CTACTTCAATGAGTGTGGAGAGTCAAGTGTATTTATAGCAGCCATTAAGCAGTGA	5340
Db	5281	CTACTTCAATGAGTGTGGAGAGTCAAGTGTATTTATAGCAGCCATTAAGCAGTGA	5340
Qy	5341	CGATATACATTTTCTCTACAGAAAAAGATTTGAGAGCTCTGGCTAAGTAAAGTCTC	5400
Db	5341	CGATATACATTTTCTCTACAGAAAAAGATTTGAGAGCTCTGGCTAAGTAAAGTCTC	5400
Qy	5401	CATAGCGGCTAAGTCTCCCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	5460
Db	5401	CATAGCGGCTAAGTCTCCCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	5460
Qy	5461	CTTGGGGTCTCTGACAGAGTAAAGGAGCAATCTTCAAAAATCTTCTTCTTCC	5520
Db	5461	CTTGGGGTCTCTGACAGAGTAAAGGAGCAATCTTCAAAAATCTTCTTCTTCC	5520

Qy	5521	TCATATGAGATCCCTACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	5580
Db	5521	TCATATGAGATCCCTACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	5580
Qy	5581	CAGCGGTTTGGAAAAAGAAATTTTGAATTAACATGTCTAGCTTACCTCTCT	5640
Db	5581	CAGCGGTTTGGAAAAAGAAATTTTGAATTAACATGTCTAGCTTACCTCTCTCT	5640
Qy	5641	CCAGCATTTTGGTTTAAATATGCAATTAACCTGCTAGATTTTGAATGAGAGGCT	5700
Db	5641	CCAGCATTTTGGTTTAAATATGCAATTAACCTGCTAGATTTTGAATGAGAGGCT	5700
Qy	5701	TGGGTATTAACCGAGAACAAAGGATTAATTAATTAACCTGCTAGATTTTGAAG	5760
Db	5701	TGGGTATTAACCGAGAACAAAGGATTAATTAATTAACCTGCTAGATTTTGAAG	5760
Qy	5761	ACTGCAAGCTGTCAAAAACAAAAGGCTTAACCAAAATTAAGTAAAGTAAAGT	5820
Db	5761	ACTGCAAGCTGTCAAAAACAAAAGGCTTAACCAAAATTAAGTAAAGTAAAGT	5820
Qy	5821	GCCAGCAGGCGCAGCAGAGGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	5880
Db	5821	GCCAGCAGGCGCAGCAGAGGATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	5880
Qy	5881	ACTGAGAGCAACTGCTTTGAAATGACAGCACTTGTGCAATTTCTTTGTTCAGAA	5940
Db	5881	ACTGAGAGCAACTGCTTTGAAATGACAGCACTTGTGCAATTTCTTTGTTCAGAA	5940
Qy	5941	TGCGTATGAGCGGTGCTTGGGAGAGTCTTCTGATTAAGGCACTTCTTTCTCTCTC	6000
Db	5941	TGCGTATGAGCGGTGCTTGGGAGAGTCTTCTGATTAAGGCACTTCTTTCTCTCTC	6000
Qy	6001	TCCTCATCTCTCTAAGATCTCTCCATGCTGTAAATCCCAATGAAGTAAAGTAAAGT	6060
Db	6001	TCCTCATCTCTCTAAGATCTCTCCATGCTGTAAATCCCAATGAAGTAAAGTAAAGT	6060
Qy	6061	ATGAATTCATGCTAGTAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	6120
Db	6061	ATGAATTCATGCTAGTAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	6120
Qy	6121	ATGAGAGCTTATTTATTTTGTCTCTCATATGAGTCTTCTCATATGCAATTCATCC	6180
Db	6121	ATGAGAGCTTATTTATTTTGTCTCTCATATGAGTCTTCTCATATGCAATTCATCC	6180
Qy	6181	ACCAGCAGCAATTAAGTGAAGAGGCTGTGGATGAAGAGGCTTCTTCAAGCTTACG	6240
Db	6181	ACCAGCAGCAATTAAGTGAAGAGGCTGTGGATGAAGAGGCTTCTTCAAGCTTACG	6240
Qy	6241	TTCTTCTTGAAGGCTACAGGAAATGCTGAGAGCTTGAATTAACCTGCGGGTAAAG	6300
Db	6241	TTCTTCTTGAAGGCTACAGGAAATGCTGAGAGCTTGAATTAACCTGCGGGTAAAG	6300
Qy	6301	AGTTCAGTCTCTGCTGAGAGCTTAACCGCATCTTAACCGCTTCTGAGACATCTT	6360
Db	6301	AGTTCAGTCTCTGCTGAGAGCTTAACCGCATCTTAACCGCTTCTGAGACATCTT	6360
Qy	6361	AGGACCAATTAAGGCTATCTGAGGCTTTTCTCTGCTGCTGCTGCTGCTGCTGCT	6420
Db	6361	AGGACCAATTAAGGCTATCTGAGGCTTTTCTCTGCTGCTGCTGCTGCTGCTGCT	6420
Qy	6421	CACATTTTCACTGCTCCAGGCTTAACCAAGATTAACAGCTGATTTTCTTCTAGGCC	6480
Db	6421	CACATTTTCACTGCTCCAGGCTTAACCAAGATTAACAGCTGATTTTCTTCTAGGCC	6480
Qy	6481	ACATTAATTAATTTGACCTGCTGATATTTCTCTATATGATTTTCTTCTTCCCA	6540
Db	6481	ACATTAATTAATTTGACCTGCTGATATTTCTCTATATGATTTTCTTCTTCCCA	6540
Qy	6541	CTGTTTAAACCCCTTAAGGATTCAGAACAACTAATATATGATTTGATTTGGA	6600
Db	6541	CTGTTTAAACCCCTTAAGGATTCAGAACAACTAATATATGATTTGATTTGGA	6600

QY 6601 AGGGSCCTTAAACATCATTCATTTCCAAACCCCTGTGCATAGGGCTGCTTGCACCCACTGG 6660
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Db 6601 AGGGSCCTTAAACATCATTCATTTCCAAACCCCTGTGCATAGGGCTGCTTGCACCCACTGG 6660
QY 6661 CTGAGGCTGCCCCAGGSCCCCATTCACAGCCCTGGCTTGGACACCTCCAGGGATGGGACCC 6720
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Db 6661 CTGAGGCTGCCCCAGGSCCCCATTCACAGCCCTGGCTTGGACACCTCCAGGGATGGGACCC 6720
QY 6721 ACAGCTTCTGCGGAGGCTGTGGCAACACCTCACACCTCTGGSTAAAGAAATCTCTGT 6780
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Db 6721 ACAGCTTCTGCGGAGGCTGTGGCAACACCTCACACCTCTGGSTAAAGAAATCTCTGT 6780
QY 6781 TTAACATCTAATCTAATCTCTCTCTTTTAAAGTAAAGCCATTCCTCTTTTCCCGTTG 6840
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Db 6781 TTAACATCTAATCTAATCTCTCTCTTTTAAAGTAAAGCCATTCCTCTTTTCCCGTTG 6840
QY 6841 CTATCTGTCCAGAAATGTGTATTTGGTCTCCCTCTGCTTAAAGCAGCACTACTGAA 6900
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Db 6841 CTATCTGTCCAGAAATGTGTATTTGGTCTCCCTCTGCTTAAAGCAGCACTACTGAA 6900
QY 6901 GGCTGACAGTGGCTGCCCAAGCCCTCTCTCTCCAGGAGCAACCAAGCCAGCTCTT 6960
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QY 7021 CAGGCTCTTCTGTGAGGCCCCAGGCTGTGATGACAGTACTTCAGATGGGGCTTACAAAG 7080
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Db 7021 CAGGCTCTTCTGTGAGGCCCCAGGCTGTGATGACAGTACTTCAGATGGGGCTTACAAAG 7080
QY 7081 GAGAGGAGATGGGAGCAATGGCTTACCCCTCCCTGGCTGGGCCCCCTGTTTGAATGAG 7140
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Db 7081 GAGAGGAGATGGGAGCAATGGCTTACCCCTCCCTGGCTGGGCCCCCTGTTTGAATGAG 7140
QY 7141 CCCAGGCTACTGTGAGCCCTTTCAGGCTCCACAGACCCTTGTGATTTGTGTCAAGCTTTT 7200
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Db 7141 CCCAGGCTACTGTGAGCCCTTTCAGGCTCCACAGACCCTTGTGATTTGTGTCAAGCTTTT 7200
QY 7201 CATCCACAGAAACCCAGCTTCTGTATATCTTCTGCTCAGCTTCTGTGAAGCTTGT 7260
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regulatory regions and complete cds.
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 1 (bases 1 to 18343)
 Chong, S., Riggs, A.D. and Bonifer, C.
 The chicken lysozyme chromatin domain contains a second, widely
 expressed gene
 Nucleic Acids Res. 30 (2), 463-467 (2002)
 JOURNAL
 MEDLINE
 PUBMED
 11788708
 21648904
 REFERENCE
 2 (bases 1 to 18343)
 Bonifer, C. and Sippel, A.E.
 Direct Submission
 Submitted (13-AUG-2001) Molecular Medicine Unit, University of
 Leeds, Beckett Street, Leeds LS9 7TF, UK
 JOURNAL
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Db 1432 GATGAGGCTTGGATAGGAGTGTGCTTGTATACATGTGATGACACTGTGCTCTT 1491
Oy 4352 TCCATCCACATCCATGATTCACATCCAGCATTTGTCAGTTATCCATATCTGCATA 4411
Db 1492 TCCATCCACATCCATGATTCACATCCAGCATTTGTCAGTTATCCATATCTGCATA 1551
Oy 4412 TCTGACATACCTGCTCTGCTGTCACCTGGTCAAGAAACAGATGATTAATCCAGCC 4471
Db 1552 TCTGACATACCTGCTCTGCTGTCACCTGGTCAAGAAACAGATGATTAATCCAGCC 1611
Oy 4472 GCCCAAGTTTGAAGATGGCAGTGTGCTTCCCTTTCCTGCTAGTAAGGATTT 4531
Db 1612 GCCCAAGTTTGAAGATGGCAGTGTGCTTCCCTTTCCTGCTAGTAAGGATTT 1667
Oy 4532 TCTCTGGCTTTGACACCTCAGCAAAATAGTCTTCTGCTTACATTTGCGCATTAATTC 4591
Db 1668 TCTCTGGCTTTGACACCTCAGCAAAATAGTCTTCTGCTTACATTTGCGCATTAATTC 1727
Oy 4592 AAATATCTTTGGAGTGGCTGCTCAGATTTGCTGCTTCACTGCTTGAAGTATGCT 4651
Db 1728 AAATATCTTTGGAGTGGCTGCTCAGATTTGCTGCTTCACTGCTTGAAGTATGCT 1787
Oy 4652 CTTAGAGTGAAGAGAGAGAGAGATGTTGGCCGAGTTCCTGATGAACACACCTC 4711
Db 1788 CTTAGAGTGAAGAGAGAGAGAGATGTTGGCCGAGTTCCTGATGAACACACCTC 1847
Oy 4712 TGAATTA--TGGCCAAAGGTGGGTGCTTCTGAGGAACGGGACGCTTTCCTGTA 4770
Db 1848 TGAATTAATTTGGCCAAAGGTGGGTGCTTCTGAGGAACGGGACGCTTTCCTGTA 1907
Oy 4771 AGCAAGGACCTGCGGAGTTCAGTATTTTGAACATGATGCTGAACCTGGGCTTAA 4830
Db 1908 AGCAAGGACCTGCGGAGTTCAGTATTTTGAACATGATGCTGAACCTGGGCTTAA 1967
Oy 4831 GCAGATTCCTTAGTTCCTGCTACTTCTTCTCTTGGCAGTCAATTTATTTCTGAC 4890
Db 1968 GCAGATTCCTTAGTTCCTGCTACTTCTTCTCTTGGCAGTCAATTTATTTCTGAC 2027
Oy 4891 AGACAACAGCCACCCCACTCAGGCTTGAAGATATGTGGCTGCTGGGTGTGTA 4950
Db 2028 AGACAACAGCCACCCCACTCAGGCTTGAAGATATGTGGCTGCTGGGTGTGTA 2087
Oy 4951 CAGCTGCGCTTGTGAAAGGGGATTAAAGGGGACCACTTATCCCAAGAGATTCCTC 5010
Db 2088 CAGCTGCGCTTGTGAAAGGGGATTAAAGGGGACCACTTATCCCAAGAGATTCCTC 2147
Oy 5011 ATTCAATGATCAAGCTGTGAAGAACTTGGGCTCCAAACCTCAAAACATTAATTTGAGTACG 5070
Db 2148 ATTCAATGATCAAGCTGTGAAGAACTTGGGCTCCAAACCTCAAAACATTAATTTGAGTACG 2207
Oy 5071 AATGTAATTTAAACTGTCAATTCGATTCCTTAAGTCATTTTACTGTGACTGTGACATG 5130
Db 2208 AATGTAATTTAAACTGTCAATTCGATTCCTTAAGTCATTTTACTGTGACTGTGACATG 2267
Oy 5131 TAGGTGCGAGCTCCCATCTTCTCAAAAGCACATGATGAGAGATGAATGAAGAC 5190
Db 2268 TAGGTGCGAGCTCCCATCTTCTCAAAAGCACATGATGAGAGATGAATGAAGAC 2327
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Qy	5191	CGATTTCGAAACAACCAACGAGAGTGTCCGGAAGAAACGTATGGAAATATATGATGAATTC	5250
Db	2328	CGATTTTCGAAACAACCAACGAGAGTGTCCGGAAGAAACGTATGGAAATAA--GCATGAATTC	2386
Qy	5251	TGTGTGTGACATTTTTTTTTTAAATACATTAACACTACTCTCAATGAGTGTGGACAGAGTCAGT	5310
Db	2387	TGTGTGTGACATTTTTTTTTTAAATACATTAACACTACTCTCAAT-----AAGGTCACT	2436
Qy	5311	GTTTTATTTACAGCCATTAACACGAGTGTAGCGAGTACCATTTTTTCTCTACAGAAAAACG	5370
Db	2437	GTTTTATTTACAGCCATTAACACGAGTGTAGCGAGTACCATTTTTTCTCTACAGAAAAACG	2496
Qy	5371	ATTCTGAGCTCTGCTGATAGATATATAGTTCTCCATATAGCGGTGTAGCTGCCCTCTGGCTGCC	5430
Db	2497	ATTCTGAGCTCTGCTGATAGATATATAGTTCTCCATATAGCGGTGTAGCTGCCCTCTGGCTGCC	2556
Qy	5431	TGCCATCTCAGCTGG-----AGTCAGTGCCTATTTCTGGGGTTTCTCTCACAGCAGTA	5485
Db	2557	TGCCATCTCAGCTGGAGTGTGAGTGTGCATTTCTGGGGTTTCTCTCACAGCAGTA	2616
Qy	5486	ATGGGACAATACCTTCACAAAA-----TCTTTTCTTTTCTGTCTATGTGGATCCCTAC	5539
Db	2617	ATGGGACAATACCTTCACAAAAATTTCTTTTCTTTTCTCTGTCTATGTGGATCCCTAC	2676
Qy	5540	TGTCCTCCCTGGTTTATACCTTACCTTACCCCTGACGTGTCCATTCAGCGGTTTGGAAAAAGAA	5599
Db	2677	TGTCCTCCCTGGTTTATACCTTACCTTACCCCTGACGTGTCCATTCAGCGGTTTGGAAAAAGAA	2736
Qy	5600	AAAGAAATTTGGAAATAAACAATGTCTACCTTATCACCTCTCCACAGCATTTTGGTTTTAA	5659
Db	2737	AAAGAAATTTGGAAATAAACAATGTCTACCTTATCACCTCTCCACAGCATTTTGGTTTTAA	2796
Qy	5660	TTATGCTAATAACAGGCTTATGATTTGGAAATAGAGGGGGTTGGGTGTATTACAGAGAA	5719
Db	2797	TTATGCTAATAACAGGCTTATGATTTGGAAATAGAGGGGGTTGGGTGTATTACAGAGAA	2856
Qy	5720	CAAAAGGAAGCTTATATATAAATCAAGTCTTTTATTTAGAAACTGGACAGCTGTCAAAA	5779
Db	2857	CAAAAGGAAGCTTATATATAAATCAAGTCTTTTATTTAGAAACTGGACAGCTGTCAAAA	2916
Qy	5780	CAAAAAAGCCCTTACACCAAAATTAAGTAAGAACCGGCTTATACGACAGAGGCGACGACGA	5839
Db	2917	CAAAAAAGCCCTTACACCAAAATTAAGTAAGTAAGAACCGGCTTATACGACAGAGGCGACGACGA	2976
Qy	5840	GGGATGTGTGACACTGTGTGGCACTATGCGACAGGCGCTGTGTGACTGTGAGACCACTGCTT	5899
Db	2977	GGGATGTGTGACACTGTGTGGCACTATGCGACAGGCGCTGTGTGACTGTGAGACCACTGCTT	3036
Qy	5900	TGGAAATGACAGCACTTGGTGTGCAATTTCTTTGTTCACAAATGCGTAAAGCGTGTCTG	5959
Db	3037	TGGAAATGACAGCACTTGGTGTGCAATTTCTTTGTTCACAAAGCGCTAAGCGTGTCTG	3096
Qy	5960	GGCAGAGTTTTCTAGATTAGAGCCACTTCTTTTCTCTCTCCATCTTCTCTAAGCAT	6019
Db	3097	GTCAGACGTTTTCTAGATTAGAGCCACTTCTTTTCTCTCTCTCTCATTTCTCTAAGCAT	3156
Qy	6020	GTCCTCATGCTGTATATCCAGTCAAGTGAAGGTTTCAAACAATGAATCATCACTGATAGG	6079
Db	3157	GTCCTCATGCTGTATATCCAGTCAAGTGAAGGTTTCAAACAATGAATCATCACTGATAGG	3216
Qy	6080	ATTCTCGGTGGATCAAAATCTTTGTGTGAGAGCTTATAAA--TATGGAAGCTTATTATT	6137
Db	3217	ATTCTCGGTGGATCAAAATCTTTGTGTGAGAGCTTATAAAATATGTAAGCTTATTATT	3276
Qy	6138	TTTTCTCTTTCATATACGTCTTCTCTATAGACAATTCACATCCACACACAG--CAATTTAA	6196
Db	3277	TTTTCTCTTTCATATACGTCTTCTCTATAGACAATTCACATCCACACACAGCAATTTAA	3356
Qy	6197	GGTGAAGAGGCTGTGGGATGAAGAGGCTTCTAGCTTTTACGTTCTTCTCTTGTGACAGC	6256
Db	3337	GGTGAAGAGGCTGTGGGATGAAGAGGCTTCTAGCTTTTACGTTCTTCTCTTGTGACAGC	3396

QY	6257	CACAGAAAATGCTGAGAGCTGTGAGATACAGCCTGGGTAAAGAGTTGAGTCTCTCTCT	6316
Db	3397	CACAGAAAATGCTGAGAGCTGTGAGATACAGCCT - GGGTAAAGAGTTGAGTCTCTCTCT	3455
QY	6317	GGGACAGTAAACCACTCTTATTAACCCCTTACAGCTCATCTTATAGAACAAATAGGGCT	6376
Db	3456	GGGACAGTAAACCACTCTTATTAACCCCTTACAGCTCATCTTATAGACTTA - GGCTTC	3514
QY	6377	TATCTGGGGTTTTGTTCCTGCTGTCTCTCTGAGAGCTATCTACATTTTCACTGCTC	6436
Db	3515	TATCTGGGGTTTTGTTCCTGCTGTCTCTCTGAGGACATGAGCCAAAGSTAGTGCA	3574
QY	6437	CCAGGCTTACAAACCAAGATACAGCCTGATTTTTTCTAGGCCACATTTACATAAATTG	6496
Db	3575	TGTGCTGGAGAGACTGTGTATTACTTAAGTGTCCACACTTCGGCTCTCTGCGCGCTGG	3634
QY	6497	ACCTGGTA - CCAATATGTTCTCATATATGTTATTTCTCCCACTGTTTAAACCTC	6555
Db	3635	CGTTTCCAGGTACCATATGCTCTTATATATATATTTCTCCCACTGTTTAAACCTC -	3693
QY	6556	TAAGCATTTGGAACCACTAGAAATCATAGATGTTTGGATTGGAAGGGCCCTTAAACAT	6615
Db	3694	TAAGCATTTGGAACCACTAGAAATCATAGATGTTTGGATTGGAAGGGCCCTTAAATAT	3753
QY	6616	CATCCATTTCCAACCTCTGTCATAGGGCTGTTGCCACCCTAGCTCAGGCTGCCAGG	6675
Db	3754	CATCCATTTCCAACCTCTGTCATAGGGCTGTTGCCACCCTAGGCTCAGGCTGCCAGG	3813
QY	6676	GCCCCATCCACCTGGGCTTGAGACCTCCAGGGAATGGGGACCCACAGCTCTCTGGG	6735
Db	3814	GCCCCATCCACCTGGGCTTGAGACCTCCAGGGAATGGGGACCCACAGCTCTCTGGG	3873
QY	6736	AGCCGTGCCCAACACCTACACACTCTCTGGGTAAAGAAATTCCTTTTAACATCTATGTA	6795
Db	3874	AGCCGTGCCCAACACCTACACACTCTCTGNNNGA - - - - - ATTCNNNNNNNNCTNRTCTA	3928
QY	6796	AATCTCTCTCTTTAGTTTAAAGCAATTCCTTTTCCGTTGCTATCTGCCAAGA	6855
Db	3929	GATCTCTCTCTTTTAAAGTAAAGCCATTCCTTTTCTGTGTATCTGTCCAAAGAA	3988
QY	6856	ATGTATTTGG - TCTCCCTCTGCTTATAGCAGGAAGTACGGAAGGCTGCAGTAGAGT	6914
Db	3988	ATGTATTTGGTTCCTCTCTGCTTATAGCAGGAAGTACGGAAGGCTGCAGTAGAGT	4048
QY	6915	CTCCCAACAGCTCTCTCTCTCCAGGCTGAACACCCACAGCTCTTCCAGCTCTCTG -	6973
Db	4049	CTCCCAACAGCTCTCTCTCTCTCCAGGCTGAACACCCACAGCTCTCTGCTTGTAGT	4108
QY	6974	TAGAGATCATTTAGTGCCCTCTCTGAGACCATTCACAGTTCACAGGCTTCTTGG	7033
Db	4109	TAGAGATCATTTAGTGCCCTCTCTCTAGGCCATTCACAGTTCACAGGCTTCTTGG	4168
QY	7034	TGGACCCCAAGTCTGATGATCACTTCAGATGGGGCTTACAAAGCAGAGCAGATGG	7093
Db	4169	TGGACCCCAAGTCTGATGATCACTTCAGATGGGGCTTACAAAGCAGAGCAGATGG	4228
QY	7094	GGACATGCTTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	7153
Db	4229	GGACATGCTTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	4287
QY	7154	TGGCCTTTCAGGCTCCAGAACCCCTTGATTTGTCTCAAGCTTTTCACTCCACAGAAC	7213
Db	4288	T - GCTTTTCAGGCTCCAGAACCCCTTGAT - - - - - TGGCAAGCTTCACACACAGACTAA	4340
QY	7214	CCAGGCTCTCTGTTAACTTCTGCTGCT - ACTTGTAGCTGTTTTCAGAGACTTC	7272
Db	4341	C - - - - - TGTGTTAAATACTTCTGCTGCTCAACTTGTAACTTGTTCAGAGAACTTC	4394
QY	7273	CATCTTTAGAGCAGACTGTGTTACACTACACTACGCTGCTTCTGATATATACATTTCA	7332
Db	4395	CATCTTTAGAGCAGACTGTGTTACACTACACTACGCTGCTTCTGATATATACATTTCA	4454
QY	7333	GTCTATGTTTCTTAACAGAGATATGTTTCTCTTAACAAATAATCTGAGAT	7392

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Db 4455 GTTCATGTTCTCGTAACAGGACAGAAATATGATTCCTCAACAAATAATATGAGAAAT 4514
OY 7393 TCCATAGTCATCTCAGTAGAGGTTTTCATGGCAGTATTAGCATATGATTAATTTGGTGA 7452
Db 4515 TCCATAGTCATCTCAGTAGAGGTTTTCATGGCAGTATTAGCATATGATTAATTTGGTGA 4574
OY 7453 AGTACCTTCCAAAGCTGCGGCCCTGCCATAAATCTGTATTTGGGATCAGTTACCTTTGGG 7512
Db 4575 AGTACCTTCCAAAGCTGCGGCCCTGCCATAAATCTGTATTTGGGATCAGTTACCTTTGGG 4634
OY 7513 GTAACCTTTGATCTGCAGAGAACCTTGGGGTTCTGATGTCTTCAGTCTGCTGT 7572
Db 4635 GTAACCTTTGATCTGCAGAGAACCTTGGGGTTCTGATGTCTTCAGTCTGCTGT 4694
OY 7573 CTGACTGCACATTTTCTAGATCACCAGTTGTCCTGTACAACTTCCCTGCTCCATC 7632
Db 4695 CTGACTGCACATTTTCTAGATCACCAGTTGTCCTGTACAACTTCCCTGCTCCATC 4754
OY 7633 CTTTCCCAAGCTTGTATCTTTGACAAATACAGGCTATTTTGTGTTGCTTCAGAGCCA 7692
Db 4755 CTTTCCCAAGCTTGTATCTTTGACAAATACAGGCTATTTTGTGTTGCTTCAGAGCCA 4814
OY 7693 TTTAATTTCTGAGTGCATCTTGTCTGTGATGCGACCTGGAACAGGATTTTCCAGCAGTC 7752
Db 4815 TTTAATTTCTGAGTGCATCTTGTCTGTGATGCGACCTGGAACAGGATTTTCCAGCAGTC 4874
OY 7753 TTGCAAAAGACATCTAGCTGAAACCTTTCTGCCATTCATATTTTACAGTTCTTCTG 7812
Db 4875 TTGCAAAAGACATCTAGCTGAAACCTTTCTGCCATTCATATTTTACAGTTCTTCTG 4934
OY 7813 TTTGAGGAGGACCATTAATTTACTAGAACTGCTCAGTCAAGTTTATGCAATTTTATAC 7872
Db 4935 TTTGAGGAGGACCATTAATTTACTAGAACTGCTCAGTCAAGTTTATGCAATTTTATAC 4994
OY 7873 TTTCTATTATGACTACTTTTGTGATACATACAGACAGCATATTTTGTGGGATTTTCA 7932
Db 4995 TTTCTATTATGACTACTTTTGTGATACATACAGACAGCATATTTTGTGGGATTTTCA 5054
OY 7933 CAGTGTCTGTGTCTCTTGCATATGATGTTTACTGTATCTTCCGTTATTAACCTTGGCAAT 7992
Db 5055 CAGTGTCTGTGTCTCTTGCATATGATGTTTACTGTATCTTCCGTTATTAACCTTGGCAAT 5114
OY 7993 CTGCCACCTGCCCATTCACAAAGAAAGATTTCTTTTATTTACTTCTCTTCCAGCAAT 8052
Db 5115 CTGCCACCTGCCCATTCACAAAGAAAGATTTCTTTTATTTACTTCTCTTCCAGCAAT 5174
OY 8053 AAACAATATGTAGAAAGCCCAAAACAAGAACTTGTGGGAGGCTGCCATCAAGGAGAGA 8112
Db 5175 AAACAATATGTAGAAAGCCCAAAACAAGAACTTGTGGGAGGCTGCCATCAAGGAGAGA 5234
OY 8113 CAGCTGAAGGTTGTGATCTCAATAGAAATTAATAAGCTGTGTGACAGAT 8172
Db 5235 CAGCTGAAGGTTGTGATCTCAATAGAAATTAATAAGCTGTGTGACAGAT 5294
OY 8173 TTTGCTGATTTATACAGGACAGGCCCAAGCCAGAGAGGCTGTCTGCCAAAGGCACTTGC 8232
Db 5295 TTTGCTGATTTATACAGGACAGGCCCAAGCCAGAGAGGCTGTCTGCCAAAGGCACTTGC 5354
OY 8233 AGTCCCTGTTTGTAAAGTAAAGTCAATTTTCTGATGAAATGCGTGGAGAAATCA 8292
Db 5355 AGTCCCTGTTTGTAAAGTAAAGTCAATTTTCTGATGAAATGCGTGGAGAAATCA 5414
OY 8293 TGATGACAGTTCTTGTCTGTTTACTATGATGTAAGATCTAAATAGAGACAGCAAAAGTAAC 8352
Db 5415 TGATGACAGTTCTTGTCTGTTTACTATGATGTAAGATCTAAATAGAGACAGCAAAAGTAAC 5474
OY 8353 ACTGTCTCTAGTGTCTGTCTGTCTATCCAGACAGGATGCGACTGCAACCAAGATGAG 8412
Db 5475 ACTGTCTCTAGTGTCTGTCTGTCTATCCAGACAGGATGCGACTGCAACCAAGATGAG 5534
OY 8413 GGATGCTCCCAAGCTGAGGATGCTGGGAGTAACAGTGGGGCCATGCTGCTCTCAT 8472
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Db 5535 GGATGCTCCCAAGCTGAGGATGCTGGGAGTAAACAGTGGGTCCATGCTGCTGCTCAT 5594
OY 8473 TAGCATCACCCTGAGCCCTCACCAGCCCATCAGAAAGATCATCCAAAGCTGAGAAAGTTG 8532
Db 5595 TAGCATCACCCTGAGCCCTCACCAGCCCATCAGAAAGATCATCCAAAGCTGAGAAAGTTG 5654
OY 8533 CTCATCTTCTTACATCATCAAAACCTTTGGCCTGATCTGATGTGCTCCGATGCTTAAATG 8592
Db 5655 CTCATCTTCTTACATCATCAAAACCTTTGGCCTGATCTGATGTGCTCCGATGCTTAAATG 5714
OY 8593 TGGTCACTACATCTTTATTTTCTATGATTTCAAGTCAAGAACCTCCGATCAGAGAGA 8652
Db 5715 TGGTCACTACATCTTTATTTTCTATGATTTCAAGTCAAGAACCTCCGATCAGAGAGA 5774
OY 8653 ACACATAGTGGGAATGTATACCTCAGCTCCAAAGCCAGATCTTCTCATATGATCATGAT 8712
Db 5775 ACACATAGTGGGAATGTATACCTCAGCTCCAAAGCCAGATCTTCTCATATGATCATGAT 5834
OY 8713 GCTACTAGGAAGTGTGTGTGTGATGTAGAAATGTGCTTTGTTATTTTCTTCTG 8772
Db 5835 GCTACTAGGAAGTGTGTGTGTGATGTAGAAATGTGCTTTGTTATTTTCTTCTG 5894
OY 8773 CTGTGAGGAACATTTTGAATACCAAGAAAGAAAGTGCCTTCTGTCATGGAGGA 8832
Db 5895 CTGTGAGGAACATTTTGAATACCAAGAAAGAAAGTGCCTTCTGTCATGGAGGA 5954
OY 8833 GTTGTACACTTGCAGAAATTAAGGATGACGTCCCAATGTTTATATATCAGAGTCTGAA 8892
Db 5955 GTTGTACACTTGCAGAAATTAAGGATGACGTCCCAATGTTTATATCAGAGTCTGAA 6014
OY 8893 GGAGGATCAGAAACCTGTGTATACAAATTTTACAGCTTCTGAAATGCAAGCTTTGAAAGCTG 8952
Db 6015 GGAGGATCAGAAACCTGTGTATACAAATTTTACAGCTTCTGAAATGCAAGCTTTGAAAGCTG 6074
OY 8953 TTTCTGCGCCGAGGACGTACTAGTCAAGAACCTTCCGAAACAGGAACAAATGCTTCAAGGT 9012
Db 6075 TTTCTGCGCCGAGGACGTACTAGTCAAGAACCTTCCGAAACAGGAACAAATGCTTCAAGGT 6134
OY 9013 GCAGGAGGAGAAACCTTGGCCATCATGAAGTGAATTAACACTGCCGTGAAGGAAT 9072
Db 6135 GCAGGAGGAGAAACCTTGGCCATCATG - AAGTGAATTAACACTGCCGTGAAGGAAT 6193
OY 9073 CCAGCTCTGTTTGAAGCAGTGTGTGACACCTCCACACCTGAAACAAGATTTATTTTAT 9132
Db 6194 CCAGCTCTGTTTGAAGCAGTGTGTGACACCTCCACACCTGAAACAAGATTTATTTAT 6253
OY 9133 AGGACTTCCAGGAAGATCTTCTTCTTAAAGCTTTTAAATTTATGTAACATCTCCAGTTGAC 9192
Db 6254 AGGACTT - CAGGAAGATCTTCTTCTTAAAGCTTTTAAATTTATGTAACATCTCCAGTTGAC 6312
OY 9193 AGATGACTATGACTACTGACAGGAGATGAGAACTAGCTGGGAATTTTCTGTTTGACC 9252
Db 6313 AGATGACTATGACTACTGACAGGAGATGAGAACTAGCTGGGAATTTTCTGTTTGACC 6372
OY 9253 ACCATGAGATCACCATTCTTACTGTATTTGGAATTAATTTTGAATTTGCAAGC 9312
Db 6373 ACCATGAGATCACCATTCTTACTGTATTTGGAATTAATTTTGAATTTGCAAGC 6432
OY 9313 AGGAGTTAGCGAAGATCTTCAATTTTCTCATGTGTGTGACACAGTCTGCTGATGAA 9372
Db 6433 AGGAGTTAGCGAAGATCTTCAATTTTCTCATGTGTGTGTGACACAGTCTGCTGATGAA 6492
OY 9373 ACTGTCTTACAAAGAGAGATTAATAATCATAGGATTAATAATCTAAGTTTGAAGCA 9432
Db 6493 ACTGTCTTACAAAGAGAGATTAATAATCATAGGATTAATAATCTAAGTTTGAAGCA 6552
OY 9433 ATGAGGTTTATGCTGATTTTGAATGAAGAAATTTAGACCTTACTGATAGCTATGCTA 9492
Db 6553 ATGAGGTTTATGCTGATTTTGAATGAAGAAATTTAGACCTTACTGATAGCTATGCTA 6612
OY 9493 TTTAGCTGCTTTTGTGTTAGTTACTTATGACCCAGCTGAGTCAAG - TATGAACTCA 9551
Db 6613 TTTAGCTGCTTTTGTGTTAGTTACTTATGACCCAGCTGAGTCAAGTATGAACTCA 6672
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QY	9552	GGTCTCTGGGCTACTGCGCATGGATTGATTACATCAACGTAAATTTTACGAGTGATTTA	9611
Db	6673	GGCTCTCCAGGCTACTGGCATGGATTGATTACATCAACTGTAATTTTACGAGTGATTTA	6732
QY	9612	GGGTTTTATGAGTACTTTTGGAGTAATTCATTTAGGGTATAGTAATGTAATCTCA - GGGAAA	9670
Db	6733	GGGTTTATGAGTACTTTTGTAGCAAAATCATAGGTTAGTAATGTTAATCTTAGGGGAAA	6792
QY	9671	AAAAAAAAAGCCAAACCTTGACACACATCCACAGTCAGGTGGAAATCAAGATCCACAGTC	9730
Db	6793	AAAAAAAAAGCCAAACCTTGACACACATCCACAGTCAGGTGGAAATCAAGATCCACAGTC	8852
QY	9731	AGTCGGGTCCCAAGAAACAGAGGACACTCTTCTCTTAAGAACCTTTATATGACAGGGCTTCAA	9790
Db	6853	AGTCGGGTCCCAAGAAACAGAGGACACTCTTCTCTTAAGAACCTTTATATGACAGGGCTTCAA	6912
QY	9791	GATTAACGATGTTATATCAGAAAGACTTTCATCTTGCGCACAGTTCCAGTGAAGCAATCCT	9850
Db	6913	GGTAACGATGTTATATCAGAAAGACTTTCATCTTGCGCACAGTTCCAGTGAAGCAATCCT	6972
QY	9851	GGAAATTTTCTCTCCGCTGCACAGTTCACATCCACAGTTGTACAGTTCTGGACACTTTT	9910
Db	6973	GGAAATTTTCTCTCCGCTGCACAGTTCACATCCACAGTTGTACAGTTCTGGACACTTTT	7032
QY	9911	TGGGTTCAGGGCGGTGATTCAGAGAGCGAAGTTCACAGTATGGTCAAGGAGAGCGCTGACCG	9970
Db	7033	TGGGTTCAGGGCGGTGATTCAGAGAGCGAAGTTCACAGTATGGTCAAGGAGAGCGCTGACCG	7092
QY	9971	TCCCAACTCACTCACTCAACAACAAAGCGGAACCAACAAGATGGCTTTTGTGAAATTTGC	10030
Db	7093	TCCCAACTCACTCACTCAACAACAAAGCGGAACCAACAAGATGGCTTTTGTGAAATTTGC	7152
QY	10031	AGTGTGCCCCAGAG36GGCTGCACACTACTGTGATTGACACAGAGGCAACATTAATCTCA	10099
Db	7153	AGTGTGCCCCAGAG36GGCTGCACACTACTGTGATTGACACAGAGGCAACATTAATCTCA	7212
QY	10091	GCAAGTGCAAATTTTGCAAGCCATTAAATTTGAACCTACTACTACATGCATCAGT - AT	10141
Db	7213	GCAAGTGCAAATTTTGCAAGC - GTAATTTAACTTGATTGACTATGATGTTAGCTTAGTCATA	7270
QY	10149	CACAACTGGTTGG3CTTGGAGAGATGCAATCTAGAGGGCTCTACAGAGATAGCTACTCTCT	10207
Db	7271	GACAACTGGTTGG3CTTGGAGAGATGCAATCTAGAGGGCTCTACAGAGATAGCTACTCTCT	7330
QY	10209	AATGAGATTGCATTTTGAAGCAGAGACACTGTAAAGCTGGCGTCTCTAAAGAGCTCTCA	10267
Db	7331	AATGAGATTGCATTTTGAAGCAGAGACACTGTAAAGCTGGCGTCTCTAAAGAGCTCTCA	7390
QY	10269	AACATTAGGGTCAAATTTTCCAGTGCACATTGTGAAGTGTGCAAGTTCGCCATGCCAAAGC	10322
Db	7391	AACATTAGGGTCAAATTTTCCAGTGCACATTGTGAAGTGTGCAAGTTCGCCATGCCAAAGC	7450
QY	10329	TGCCCAACATCTTACACTCTTCCAAATGAAATCAATTTATGACAGGGTACTGCTTTCTGCCA	10388
Db	7451	TGCCCAACATCTTACACTCTTCCAAATGAAATCAATTTATGACAGGGTACTGCTTTCTGCCA	7510
QY	10389	GCA - CTGTCTCTCTCAAACTGAACCTCAACAAACAAATTTCAAGCTAGTAGAAATACAA	10447
Db	7511	GCACCTCTCTCTCTCAAACTGAACCTCAACAAACAAATTTCAAGCTAGTAGAAATACAA	7570
QY	10448	GCTTTGAAATGTCAAT - AAAAAAGTATATCTGCTTTCAAGTATTCAGCTTATTTATG - CCCA	10507
Db	7571	GCTTTGAAATGTCAAT - AAAAAAGTATATCTGCTTTCAAGTATTCAGCTTATTTATG - CCCA	7630
QY	10506	CTAGAAACATCTTGTCAAGAGCTGAACACAGCGGGCTCCAGATTAGTGTGTAACCTACTTT	10566
Db	7631	CTAGAAACATCTTGTCAAGAGCTGAACACAGCGGGCTCCAGATTAGTGTGTAACCTACTTT	7690
QY	10566	ATACATATCATAGATCATATGAATGGCT - GGGTTGGAAGGAGCCCAAGATCATATGAGA	10622
Db	7691	TACAAATCATATGATCATATGAATGGCTCGGGTTTGGAAAGGGAACCCCAAGATCATAGAG	7750

OY	10625	TCGACACCCCCCGCACAGGCAGGGCCACCAACTCTCCAGATCTGGTACTAGACCAGCAG	10684
Db	7751	TCGAACAACCCC CGCACAGGCAGGGCCACCAAC - - TCAGATCTTCTA - - AGCCAGGGCG	7806
OY	10685	CCGAGGGCTCCATTCACAACTGGGCATGGAACACTCTCAGGAAATGGGAGCATCCACAACTCT	10744
Db	7807	CCGAGGGTTCCATTCACAACTAGCTTGGAACACTTCCAAGATGGGTATCCACAACTCT	7866
OY	10745	CTGGGAGCCTGTGACAGCACCTCACACACCTCTCTGTGAAGAATCTTTCCTGACATCC	10804
Db	7867	CTGGGAGCCTGTGACAGCACCTCACACACCTCTGTGAAGAATCTTTCCTGACATCC	7926
OY	10805	AATTAAGCTTCCCTCTCTTGAGGTATTAGATCCACTGCCCTTGTGTATCATCTGTACT	10866
Db	7927	AATTAAGCCTTCCCTCTCTTGAGGTATTAGATCCACTGCCCTTGTGTATCATCTGTACT	7986
OY	10865	CTTGTAAAAAGTTGATTCCTCTCTCTTGGAAAGTTGCANATGAG - - GTCTCC	10911
Db	7987	CTTGT - AAAAGTTAGTTCTCTCTCT - TTTTGGAAAGTTGCANATGAGTCTCTTGCCTCT	8044
OY	10916	TTTGAGCCTTCTCTCTCTTCTGAGATGAGAACAGCCAGCCTCCACAGCCTGTCTTATA	10977
Db	8045	CNNNNNNNNNNNNNNNNTGCGAGGATGAGAACAGCCAGCCTCCACAGCCTGTCTTATA	8104
OY	10976	GGAGAGTGTCTCAGCCCTCTGTATCATCTTGTGGCCCTCTCTGTGACCCGCTCAAAG	11035
Db	8105	GGAGAGTGTCTCAGCCCTCTGTATCATCTTGTGGCCCTCTCTGTGACCCGCTCAAAG	8164
OY	11036	CTCCACATCTTCTCTCTACTGGGGGGCCCGCAGCCGTGAATGCATATCTCAGATGGGGCT	11099
Db	8165	CTCCACATCTTCTCTGTACTGGGGGGCCCGCAG - CTGAATGAGATATCTCAGATGGGGCT	8223
OY	11096	CAAAAGAGCAGAGTAAAGAGGGGACATCATCTTCTCTCACCCTGGTGGCAGCCCTCTCT	11155
Db	8224	CAAAAGAGCAGAGTAAAGAGGGGACATCATCTTCTCTCACCCTGGTGGCAGCCCTCTCT	8283
OY	11156	GATGGAG - CCGTGGATPACCACTGGCTTCTGTAGCTGACACTTCTCTTATCAGTTCCACT	11214
Db	8284	GATGGAGACCATGGATPACCACTGGCTTCTGTAGCTGACAACTTCTCTTATCAGTTCCACT	8343
OY	11215	ATTAAACAGAACATPACAAACAGTGTGATGGCCACTGCAGAGTTTTTCACACTTCTT	11277
Db	8344	ATTAAACAGAACATPACAAACAGTGTGATGGCCAGTGTGATTTTTTCACACTTCTT	8403
OY	11275	CATTTCGGTAGATCTTAGATGAGGAACGTGTGAAGTTGTGGCTTTCGCGTGGCTTCTCT	11334
Db	8404	CATTTCGGTAGATCTTAGATGAGGAACGTGTGAAGTTGTGGCTTTCGCGTGTCTTCTCT	8463
OY	11335	CCTCAAACTACTCTGTGCTGTATACCTTACCCCACTGGCCACAGTAATGGCTCCATGGCCCC	11394
Db	8464	TCTCAAACTACTCTGTGCTGTATACCTTACCCCACTGGCCACAGTAATGGCTCCATGGCCCC	8523
OY	11395	TGCAGCCAGGGCCCTGTATGAAACCCGGCACTGCTTCAGATGCTGTTTAATAGCACAGTAG	11455
Db	8524	TGCAGCCA - GGCCCTGATGAAACCCAGCACTGCTTCAGATGCTGTTTAATAGCACAGTAG	8582
OY	11455	ACCAAGTGGACCTATGATATACAAACAATGTTGSAATGCTTCACAGCACTTGAGAAGAA	11511
Db	8583	ACCAAGTGGACCTATGATATACAAACAATGTTGSAATGCTTCACAGCACTTGAGAAGAA	8642
OY	11515	GAGCAAAATTTGATTTGTGAGAAATGTTTTGTAAATCTGCCAATTAAAACCTGTTTAT	11577
Db	8643	GAGCAAAATTTGATTTGTGAGAAATGTTTTGTAAATCTGCCAATTAAAACCTGTTTAT	8702
OY	11575	CTACCATGSGCTGTTTTTATGCGCTGTAGTAGTGATGACACTGATGATGAACAATGGCTTAG	11634
Db	8703	CTACCATGSGCTGTTTTTATGCGCTGTAGTAGTGATGACACTGATGATGAACAATGGCTTAG	8762
OY	11635	CAGTAATAATTAACAAGCTGATATTTGCCAAGACATATATAAATTTCTCTGTGGCTTAGCCA	11699
Db	8763	CAGTAATAATTAACAAGCTGATATTTGCCAACA - - CTATAATTTCTCTGTGGCTTAGCCA	8819
OY	11695	ATGTGTACTTCCCAATTGTATTAAGAAATTTGGCAATGTTTAGACCAATGTTTGAAGTG	11754

D _b	8820	ATG -GGTCTTCCACACATGTATAGAAATTGTGGCAGTTTAGACAAATG -TTGAAGTGT			8877
O _y	11755	TGGGAATTCTCTGTATTACTCAAGAGGGCGTTTBTACAACTGTAAACACAGAGAAATCAAA			11814
D _b	8878	TGGCAAAATTTCTG -ATACCTCAGAGGGCGTTTGTACAACTGTAAACACAGAGAAATCAAA			8936
O _y	11815	AGGGCGTGGGAGGAAGTTAAAAAGAGAGCGACAGTGCAGAGAGACTTGCAGTCCCGCTGTG			11874
D _b	8937	AGGGGCTGGGAGGAAGTTAAAAAGAGAGCGAGTGCAGAGAGACTTGCAGTCCCGCTGTG			8996
O _y	11875	TGTACGACACTGGCAACAATGAGGTTTGTGTAAATGTAGTGGTTTGGTTCCTCCGCCCTGG			11934
D _b	8997	TGTACGACACTGGCAACAATGAGGTTTGTGTAAATGTAGTGGTTTGGTTCCTCCGCCCTGG			9056
O _y	11935	CTGCCTTAGGG			11945
D _b	9057	CTGCCTTAGGG			9067

RESULT 4			
LOCUS	GGGH1.		
DEFINITION	GGGH1	1668 bp	DNA
	G.gallus	lysosome gene 5'	linear
		matrix attachment region (MAR)	VRT 23-OCT-1996

ACCESSION	X98408
VERSION	X98408.1
KEYWORDS	lysozyme; matrix attachment region.
SOURCE	chicken.
ORGANISM	Gallus gallus

REFERENCE AUTHORS TITLE	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
1 (bases 1 to 1668)	
Phi-Van, L. and Stralling, W.H.	
Dissection of the ability of the chicken lysozyme gene 5' matrix	

JOURNAL	Biochemistry	35	(33),	10735-10742	(1996)
MEDLINE	96346067				
PUBMED	8718863				
REFERENCE	2	(bases 1 to 1668)			

JOURNAL Submitted (11-JUN-1996) W.H. Straeeling, Institut fuer Physiologische Chemie, Universitaets-Krankenhaus Eppendorf, Martinistrasse 52, D-20246 Hamburg, FRG

FEATURES Location/Qualifiers

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misc.feature
/ob_xref="taxon:9031"
/clone="lambda 4/2"
1.1668
/note="B-1-H1 subfragment of 5' MMR (matrix attachment
region) of bacteriophage lambda 4/2"
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upstream of the lyszyme gene promoter (see X52989 & X84223 for subfragment H1-SacI)"

QY 1 TGGCGCTTCTTTTGATTAATCACTGCTGTGATTTCATCTCTTCTGGCGATGAAGATA 60
Best Local Similarity 9/.14; P-Ref. NO. 0;
Matches 1523; Conservative 0; Mismatches 16; Indels 29; Gaps 11;

Qy	61	TAA	CAG	TCT	GAT	TAA	CAG	TCT	GAG	AA	TACT	TGG	TAT	TCT	TTC	GAT	CAG	TGT	TTT	120
Db	180	-----	TAT	AAC	AGT	CTC	TG	AG	AA	AAC	TCT	TGG	TAT	TCT	TTC	GAT	CAG	AGG	TTT	229

QY	121	ATAGTATCTTGAATATTTGGATTAAGGCTGTGTCTCTTGTCTTGCGAGACAAAGCCCA	180
Db	230	ATAAGTATGTGGATATTTGGATTAAGGCTGTGTCTCTTGTCTTGCGAGACAAAGCCCA	289
QY	181	CAGCAGGTGGTGGGGGTGGTGGCGAGCTGACATGCACAGAGAGTCTTTTGGCGTGT	240
Db	290	CAGCAGGTGGTGGTGGGGGTGGTGGCGAGCTGACATGCACAGAGAGTCTTTTGGCGTGT	348
QY	241	TTTTTT-TTTTTTTTTTTTTTAAGTAAGTGTCTTTTTCTTAAATTTTTCTACTGG	299
Db	349	TTTTTTGTGTTTTTTTTTTTAAGTAAGTGTCTTTTTCTTAAATTTTTCTACTGG	408
QY	300	ACTGTATGTTTTGCACAGTCAGAAACATTTCTTCAAAAGAAACCTTTTGGAACTGT	359
Db	409	ACTGTATGTTTTGCACAGTCAGAAACATTTCTTCAAAAGAAACCTTTTGGAACTGT	468
QY	360	CAGCCCTTTCTTTCATCCCTTTTGGCTTTCGTGCGCAATGCTTGGTGTGATGTCA	419
Db	469	CAGCCCTTTCTTTCATCCCTTTTGGCTTTCGTGCGCAATGCTTGGTGTGATGTCA	528
QY	420	TTATGAAAACGTTGATGCGAAGCTTGAGTCTTTTATTTATAGTGTGCTTGAACCTTGG	479
Db	529	TTATGAAAACGTTGATGCGAAGCTTGAGTCTTTTATTTATAGTGTGCTTGAACCTTGG	588
QY	480	ATACGTGTGTTNACAGATATACCTTAATTAAGTTTGGCGACCTTGATGCTTGA-TTTTT	538
Db	589	ATACGTGTGTATATAGATAGATACCTTAATTAAGTTTGGCGACCTTGATGCTTGAATTTT	648
QY	539	TCCCTTTGAAGTATGAGGCGCTCTCTGCTGTTTTTTTCTTGAACGTGTGAGGCTTAGAT	598
Db	649	TTCCTTTGAAGTATGAGGCGCTCTCTGCTGTTTTTTCTTCTTGAACGTGTGAGGCTTAGAT	708
QY	599	TTTTCTATGSGGATTTTTTACCTGATGATCTAGTTCATACCCAAATGCTGTAAATGTT	658
Db	709	TTTTCTATGSGGATTTTTTACCTGATGATCTAGTTCATACCCAAATGCTGTAAATGTT	768
QY	659	TTCTCTAGTTAAACATGTTGATTAACCTTGGAATTAACATGTTATATACCTGTGATCTGGT	718
Db	769	TTCTCTAGTTAAACATGTTGATTAACCTTGGAATTAACATGTTATATACCTGTGATCTGGT	828
QY	719	TTCTAGTAAATAATATATGCGATTTATAGAAATACGTAAATTCCTGATTTCC-TTTTTTTTT	777
Db	829	TTCTAGTAAATAATATATGCGATTTATAGAAATAACGTAAATTCCTGATTTCCTTTTTTTT	888
QY	778	ATCTCTATGCTCTGTGTGTATCAGGTCAAACAGACTTCACTCTATTTTATTTATAGAT	837
Db	889	ATCTCTATGCTCTGTGTGTATCAGGTCAAACAGACTTCACTCTATTTTATTTATAGAT	948
QY	838	TTTATATGCAAGTCGTGCGTGTGTTCTTGTTGGTGTAGAGTATACGCGTTAAATTCCTGTA	897
Db	949	TTTATATGCAAGTCGTGCGTGTGTTCTTGTTGGTGTAGAGTATACGCGTTAAATTCCTGTA	1008
QY	898	GCAGTGCCTCAGTAAAGCGGGGTTGTCAATGCGGTTCCAAATGTAAACGGGACGTTGGCT	957
Db	1009	GCAGTGCCTCAGTAAAGCGGGGTTGTCAATGCGGTTCCAAATGTAAACGGGACGTTT-GCT	1067
QY	958	GCTGCTTCCCGAGATCCAGGACACTAAATGCTCTGCG-ACGTAGGTAAATGCTTTC	1016
Db	1068	GCTGCTTCTCCC-AGATCCAGAGCACTAAATGCTCTGCGACACTGAGGTAAATGCTTTC	1126
QY	1017	AGATCCCAAGGGAAGTCAGATCCAGCTGATATCTTAAGAAAGATATATCTTTCTAA	1076
Db	1127	AGATCCCA-GGAAAGTGTAGATCCAGCTGATATCTTAAGAAAGATATATCTTTCTAA	1185
QY	1077	AATTTTGGCATAGAGCAACCTCATGGAATTTGTTGGAGCTTAAATTAATTTGGTA	1136
Db	1186	AATTTTGGCATAGAGCAACCTCATGGAATTTTGGAGCTTAAATTAATTTGGTA	1245
QY	1137	ACGAGGTGCTATAGTTTTTAAACACACATTTCCACATGCTTAACAGTACACAGGTTTATGCA	1196
Db	1246	ACGAGGTGCTATAGTTTTTAAACACACATTTCCACATGCTTAACAGTACACAGCATTTATGCA	1305
QY	1197	GAACTGATCCCTGATAGCTCTGTTCAGGCTTTTACGGACATGCTTTCGATGTAGCATTTGC	1256


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Db 3473 CAGCCCTTTCTTCAATCCCTTTTGTCTGTGCCCATCCCTTTGGTCTGATGCA 3532
Oy 420 TTATGGAAACGTTGATGGAAGCTTTTATTTATTTAGTGTGCTGGAAGCTTGG 479
Db 3533 TTATGGAAACGTTGATGGAAGCTTTTATTTATTTAGTGTGCTGGAAGCTTGG 3592
Oy 480 ATAGCTGTGTTACACGAGATACCTTATTAACTTAAAGCCAGCTGATCCTTTA-TTTTT 538
Db 3593 ATAGCTGTGTTACATGATACCTTATTAAAGTTAGCCAGCTGATCCTTATTATT 3652
Oy 539 TCCCTTTGAGTAGAGAGGCTCTGGTTTTCCTTTGAAACGGAGGCTTAGAT 598
Db 3653 TTCTTTGAGTAGAGAGGCTCTGGTTTTCCTTTGAAACGGAGGCTTAGAT 3712
Oy 599 TTTTCTAATGAGATTTTATACCTGATGATCTAGTTGCAATACCAATGCTTGAATTT 658
Db 3713 TTTTCTAATGAGATTTTATACCTGATGATCTAGTTGCAATACCAATGCTTGAATTT 3772
Oy 659 TTCTCTAGTTAATCATGTGTGTAACCTTCCGATTTACATGTTGTATATCTGATCTGT 718
Db 3773 TTCTCTAGTTAATCATGTGTGTAACCTTCCGATTTACATGTTGTATATCTGATCTGT 3832
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Db 3833 TTCTCTAGTTAATCATGTGTGTAACCTTCCGATTTACATGTTGTATATCTGATCTGT 3892
Oy 778 ATCTCTAGCTCTGTGTGTAACGAGTCAACAGACTTCACTCTATTTTATTTATAGAT 837
Db 3893 ATCTCTAGCTCTGTGTGTAACGAGTCAACAGACTTCACTCTATTTTATTTATAGAT 3952
Oy 838 TTTATATGAGCTCTGTGTGTGTTCTGTGTGTGAAGATACAGCTTAAATTTCTTACA 897
Db 3953 TTTATATGAGCTCTGTGTGTGTTCTGTGTGTGAAGATACAGCTTAAATTTCTTACA 4012
Oy 898 GCGATGCTCAGTAAGAGCGGCTGTGTCATGAGGTCAATGATTAAGAGCGGACGTTGGCT 957
Db 4013 GCGATGCTCAGTAAGAGCGGCTGTGTCATGAGGTCAATGATTAAGAGCGGACGTTGGCT 4071
Oy 958 GCTGCTTCCGAGATCCAGACACTAACTCTCTGCG-ACGTAGGATTAATGCGCTTC 1016
Db 4072 GCTGCTTCCGAGATCCAGACACTAACTCTCTGCGACACTGAGGTAAATGCGCTTC 4130
Oy 1017 AGATCCGAGGAGAGAGAGATCCAGTGCATATTCCTTAAAGAAAGATGATCTTCTAA 1076
Db 4131 AGATCCGAGAGAGAGATCCAGTGCATATTCCTTAAAGAAAGATGATCTTCTAA 4189
Oy 1077 AATATTTTGGCATAGGAAGCAAGTGCATGATTTGTTGGGACCTTAAATTTTGGTA 1136
Db 4190 AATATTTTGGCATAGGAAGCAAGTGCATGATTTTGGGACCTTAAATTTTGGTA 4249
Oy 1137 ACGGAGTGCATAGTTTAAACACAGTTGCAAGTGCATGCAAGAGTGCACAGCTTATGCA 1196
Db 4250 ACGGAGTGCATAGTTTAAACACAGTTGCAAGTGCATGCAAGAGTGCACAGCTTATGCA 4309
Oy 1197 GAGAGTATGCTGAGTGCCTGTGTGCAAGTGTTCAGGACAGCTCTTGCAGTAGAGATTGC 1256
Db 4310 GAGAGTATGCTGAGTGCCTGTGTGCAAGTGTTCAGGACAGCTCTTGCAGTAGAGATTGC 4361
Oy 1257 AGATGGGGGTGGGGTGTGTGTGTGTGTTCCACAGGTCGACACAGCCACCTCCGG 1316
Db 4362 AGATGGGGGTGGGGTGTGTGTGTGTGTGTTCCACAGGTCGACACAGCCACCTCCGG-6 4420
Oy 1317 AACACATCTCAACCTGCTGGTACTTTTCAAAACCATCTTAAAGCATAGTAGATAGTTACTA 1376
Db 4421 AACACATCTCAACCTGCTGGTACTTTTCAAAACCATCTTAAAGCATAGTAGATAGTTACTA 4480
Oy 1377 TGAACAACAAGAGTTCTCAGTGTGATATCTCATGAGGATGTCTTTTCCATGTTGGG 1436
Db 4481 TGAACAACAAGAGTTCTCAGTGTGATATCTCATGAGGATGTCTTTTCCATGTTGGG 4540
Oy 1437 CAAATATGATTAAGCATCTCATTTGTAATATGCACTGTGTAGTCCCTAACTCTT 1496

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Db 4541 CAAAGTATGATAAAGCATCTCATTTGTAATTAAGCACTGTGTAGTTCGTAATCTTT 4600
Oy 1497 CTATACACACACTTATTTGAGCAGAGGTAGGCTGTGTGGCCTGTGTGCTGCA 1556
Db 4601 CTATACACACACTTATTTGAGCAGAGGTAGGCTGTGTGGCCTGTGTGCTGCA 4660
Oy 1557 TCTTTTAA 1564
Db 4661 TCTTTTAA 4668

RESULT 6
CLCURVAS
LOCUS CLCURVAS 660 bp DNA linear VRT 22-OCT-1990
DEFINITION Chicken lysozyme gene intrinsically curved segment of DNA.
ACCESSION X52989
VERSION X52989.1 GI:62716
KEYWORDS curved DNA; matrix attachment region.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 660)
REFERENCE 1 (bases 1 to 660)
AUTHORS Straetling, W.H.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-1990) Straetling W.H., Physiologisch-Chemisches
Institut, Universitaets-Krankenhaus Eppendorf, Martinstr. 52,
D-2000 Hamburg, FRG
2 (bases 1 to 660)
REFERENCE von Kries, J.P., Phi-Van, L., Diekmann, S. and Straetling, W.H.
AUTHORS A non-curved chicken lysozyme 5' matrix attachment site is 3'
TITLE followed by a strongly curved DNA sequence
JOURNAL Nucleic Acids Res. 18 (13), 3881-3885 (1990)
MEDLINE 90326509
PUBMED 2374712
COMMENT Data kindly reviewed (11-AUG-1990) by Straetling W. This sequence
represents an intrinsically curved segment of the chicken lysozyme
5' matrix attachment region (MAR).
FEATURES
source 1..660
/organism="Gallus gallus"
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BASE COUNT 179 a 123 c 126 g 232 t
ORIGIN
Query Match 5.4%; Score 644.2; DB 5; Length 660;
Best Local Similarity 99.4%; Pred. No. 1.8e-141;
Matches 657; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Oy 2011 GCGCTGCTGACTTTTAAACATAGGCTGATTTGCTTCTGTACCATTTGCTCA 2070
Db 1 GCGCTGCTGACTTTTAAACATAGGCTGATTTGCTTCTGTACCATTTGCTCA 60
Oy 2071 TTCCCAATTTGCAACAAGATGTCTGGTAACTATTCAAGAAATGCTTGAATACAGC 2130
Db 61 TTCCCAATTTGCAACAAGATGTCTGGTAACTATTCAAGAAATGCTTGAATACAGC 120
Oy 2131 AAGGAGCTGTGCTGAGTTGGAATGCAAGTTGCACTGCAAAATGTCAGGAATGAGATG 2190
Db 121 AAGGAGCTGTGCTGAGTTGGAATGCAAGTTGCACTGCAAAATGTCAGGAATGAGATG 180
Oy 2191 CTCTCAGAAATGCCCAATCCCAAGAGATTTTATGTGTTATATAGTAAAGCAGTTTCTGAT 2250
Db 181 CTCTCAGAAATGCCCAATCCCAAGAG-TTTATATGTGTTATATAGTAAAGCAGTTTCTGAT 239
Oy 2251 TCCAGCAGGCCAAGAAGTCTGCTGAATGTGTGTGCGGAGACCTGTATTTCTCAACAA 2310
Db 240 TCCAGCAGGCCAAGAAGTCTGCTGAATGTGTGTGCGGAGACCTGTATTTCTCAACAA 239
Oy 2311 GGTAGATGTGATCTCTAGCACTGGGATTTTAAATACATTTTTCACAGAAAGTACTAGT 2370

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Db 300 GGTAAGATGTATCCTAGCAACGCGGATTTAATACATTTTCAGCAGAACTAGT 359
OY 2371 AATCTCTACCTTAGGATCGTTTCATCTTTTAGATGTATTGAATCTGCATA 2430
Db 360 AATCTCTACCTTAGGATCGTTTCATCTTTTAGATGTATTGAATCTGCATA 419
OY 2431 ACTTTAGCTTCAGGCTGCTTTTTCAGCCTTTAGAGAGCTTTAGCAATTTGCT 2490
Db 420 ACTTTAGCTTCAGGCTGCTTTTTCAGCCTTTAGAGAGCTTTAGCAATTTGCT 479
OY 2491 GTCCAACTTTGTGTGCTTTAACTGCAATAGTATTACCTTTATTTGAAGAAATA 2550
Db 480 GTCCAACTTTGTGTGCTTTAACTGCAATAGTATTACCTTTATTTGAAGAAATA 539
OY 2551 AGACCACTTTTATTTAAATAAATCTTTGTCTGCTCATTTTGACTGCTGATATCC 2610
Db 540 AGACCACTTTTATTTAAATAAATACTTTGTCTGCTCATTTTGACTGCTGATATCC 599
OY 2611 TTGCAGTGGCCATTTATGTCAGTTCTGTGCAATATTCAGACATCAAACTTAACGTGAGCT 2670
Db 600 TTGCAGTGGCTATTTATGTCAGTTCTGTGCAATATTCAGACATCAAACTTAACGTGAGCT 659
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Db 660 C 660

RESULT 7
CHKLSZF
LOCUS 720 bp DNA linear VRT 13-MAY-1999
DEFINITION Gallus gallus egg white lysozyme gene, partial cds.
ACCESSION J00886 V00429
VERSION J00886.1 GI:212277
KEYWORDS
SOURCE
ORGANISM Gallus gallus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 720)
Grez,M., Land,H., Glesecke,K., Schutz,G., Jung,A. and Sippel,A.E.
Multiple mRNAs are generated from the chicken lysozyme gene
JOURNAL Cell 25 (3), 743-752 (1981)
MEDLINE 82025586
PUBMED 7285117
REFERENCE
2 (bases 220 to 440)
von der Ahe,D., Janich,S., Scheiderreit,C., Renkawitz,R., Schultze,G.
and Beato,M.
Glucocorticoid and progesterone receptors bind to the same sites in
two hormonally regulated promoters
JOURNAL Nature 313 (6004), 706-709 (1985)
MEDLINE 85137874
PUBMED 2983219
REFERENCE
3 (sites)
Wojtil,S., Schrader,M. and Wittig,B.
Lack of correlation between DNA methylation and transcriptional
inactivation: the chicken lysozyme gene
Proc. Natl. Acad. Sci. U.S.A. 88 (1), 271-275 (1991)
JOURNAL 91095443
MEDLINE
PUBMED 1986375
COMMENT
On May 13, 1999 this sequence version replaced gi:63584.
FEATURES
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Query Match
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Matches 518; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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BASE COUNT 202 a 126 c 186 g 206 t
ORIGIN
OY 11424 TGGTCAGATGCTGTTTATATAGCAGATATGACCAAGTTGCACCTATGATGACAAACA 11483
Db 1 TGGTCAGATGCTGTTTATATAGCAGATATGACCAAGTTGCACCTATGATGACAAACA 60
OY 11484 ATGTGTGCTACCTTACGACCTGAGAAAGAGCCAAATTTGCATTGTGATGAGAAATGCT 11543
Db 61 ATGTGTGCTACCTTACGACCTGAGAAAGAGCCAAATTTGCATTGTGATGAGAAATGCT 120
OY 11544 TTAGTAATCTGCCAATTAACCTTGTATTACACATGAGCTGTTTATGCTGTAGT 11603
Db 121 TTAGTAATCTGCCAATTAACCTTGTATTACACATGAGCTGTTTATGCTGTAGT 180
OY 11604 AGTGTAACCTGATGATGAACAATGGCTATGCACTAAATCAAGACTGTATGATTCGAA 11663
Db 181 AGTGTAACCTGATGATGAACAATGGCTATGCACTAAATCAAGACTGTATGATTCGAA 240
OY 11664 CAGACTATTAATTCCTGCTGGCTTAGCCAGTGTGGTACTTCCCATTTGATTAAGAAA 11723
Db 241 CAGACTATTAATTCCTGCTGGCTTAGCCAGTGTGGTACTTCCCATTTGATTAAGAAA 300
OY 11724 TTTCGCAAGTTTATGAGCAATGTTTGAAGTGTGGAAATTTCTGTACTCAAGAGGCG 11783
Db 301 TTTCGCAAGTTTATGAGCAATGTTTGAAGTGTGGAAATTTCTGTACTCAAGAGGCG 360
OY 11784 TTTTGGACAACCTGTAGAACAGAGCAATCAAAAGGGGTGGAGAACTTAAGAAGAGG 11843
Db 361 TTTTGGACAACCTGTAGAACAGAGCAATCAAAAGGGGTGGAGAACTTAAGAAGAGG 420
OY 11844 CAGGTGCAAGAGAGCTTGCAGTCCCGCTGTGTAGACACTGGCAACATGAGAGCTTTTG 11903
Db 421 CAGGTGCAAGAGAGCTTGCAGTCCCGCTGTGTAGACACTGGCAACATGAGAGCTTTTG 480
OY 11904 CTATCTTGGTGTCTTGTGCTTCTGCTCCCTGGCTGCTTATAGG 11945
Db 481 CTATCTTGGTGTCTTGTGCTTCTGCTCCCTGGCTGCTGCTGCGG 522

RESULT 8
GGDNALGP
LOCUS 449 bp DNA linear VRT 11-FEB-1995
DEFINITION G.gallus lysozyme gene promoter.
ACCESSION X84223
VERSION X84223.1 GI:666995
KEYWORDS
SOURCE
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 449)
Buhmester,H., von Kries,J.P. and Straetling,W.H.
Nuclear matrix protein ARBP recognizes a novel DNA sequence motif
with high affinity
JOURNAL Biochemistry
2 (bases 1 to 449)
Straetling,W.H.
Direct Submision
Submitted (27-JAN-1995) W.H. Straetling, Institut fuer
Physiologische Chemie, Universitaets-Krankenhaus Eppendorf,
Martinistrasse 52, 20246 Hamburg, FRG
JOURNAL
MEDLINE
PUBMED
REFERENCE
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ORIGIN

Query Match 3.6%; Score 432.8; DB 5; Length 449;
Best Local Similarity 98.9%; Pred. No. 2.5e-91;
Matches 447; Conservative 0; Mismatches 2; Indels 3; Gaps 1;

QY 1564 AAGCTCTTGGAAATACACTGACTGATTGAGTCTCTTGAAGATAGTAACACTACTT 1623
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Db 1 AAGCTCTTGGAAATACACGACTGATTGAGTCTCTTGAAGATAGTAACACTACTT 60
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QY 1624 ACCCTTGATCCCAATGAATGAGCATTTCAGTTGTAAGAATTCGGCTATTGATACC 1683
|||||
Db 61 ACCCTTGATCCCAATGAATGAGCATTTCAGTTGTAAGAATTCGGCTATTGATACC 120
|||||

QY 1684 ATGTAATGTAATTTACACCCCGAGTGTGACACTTGGAAATATTCAGTAATAGACT 1743
|||||
Db 121 ATGTAATGTAATTTACACCCCGAGTGTGACACTTGGAAATATTCAGTAATAGACT 180
|||||

QY 1744 TTGGCTCACCCTCTTGTGACTGATTTTGTATATAGAAATATTTAAACGTGCATAT 1803
|||||
Db 181 TTGGCTCACCCTCTTGTGACTGATTTTGTATATAGAAATATTTAAACGTGCATAT 240
|||||

QY 1804 GATTATTCATTATGAAAGACATCTGCTGATCTTCAATGTAGAAGAAATGAGAGTG 1863
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Db 241 GATTATTCATTATGAAAGACATCTGCTGATCTTCAATGTAGAAGAAATGAGAGTG 300
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QY 1864 CGTGCGCTTTATATAATCAAGTGTGCAATTTAGTGAGGTGCTTAAAGAAAAA 1923
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Db 301 CGTGCGCTTTATATAATCAAGTGTGCAATTTAGTGAGGTGCTTAAAGAAAAA 357
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QY 1924 AAAAAAGTAATATATAAAGACAGAGTGTTTTACAAAGTAATACATTCCTATTGGTAA 1983
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Db 358 AAAAAAGTAATATATAAAGACAGAGTGTTTTACAAAGTAATACATTCCTATTGGTAA 417
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QY 1984 ACAGTTACATTTTATGAAGATTACAGCGCT 2015
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Db 418 ACAGTTACATTTTATGAAGATTACAGCGCT 449
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RESULT 9
GGLYSHRE 441 bp DNA linear VRT 06-JUL-1989
LOCUS
DEFINITION Chicken lysozyme gene promoter region with hormone responsive
element (HRE).
ACCESSION X12509
VERSION X12509.1 GI:63583
KEYWORDS hormone receptor; lysozyme; steroid hormone receptor.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 441)
Hecht,A., Berkenstam,A., Stromstedt,P.E., Gustafsson,J.A. and
Slipfel,A.E.
TITLE A progesterone responsive element maps to the far upstream steroid
dependent DNase hypersensitive site of chicken lysozyme chromatin
EMBO J. 7 (7), 2063-2073 (1988)
JOURNLT MEDLINE
MEDLINE 88328995
PUBMED 3416833
COMMENT author numbering according transcript start site -2250 to -1815;
see V00429 for lysozyme gene exon 1.
FEATURES Data kindly reviewed (17-Apr-1989) by Berkenstam A.
Location/Qualifiers

source 1..441
/organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="lambda lys30 and lambda lys31."
misc_feature 122..138
/note="glucocorticoid receptor site"
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/note="progesterone receptor site"
misc_feature 151..169
/note="progesterone receptor site"
misc_feature 153..169
/note="glucocorticoid receptor site"
misc_feature 188..220
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misc_feature 189..220
/note="progesterone receptor site"
misc_feature 254..295
/note="progesterone receptor site"
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BASE COUNT 122 a 107 c 108 g 104 t
ORIGIN

Query Match 3.5%; Score 421; DB 5; Length 441;
Best Local Similarity 98.6%; Pred. No. 1.6e-88;
Matches 435; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 9621 AGTACTTTGGCAGTAAATCATAGGGTTAGTATGTTAATCTGA-GGAAAAA 9679
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Db 1 AGTACTTTGGTGAACAAATCATAGGGTTAGTATGTTAATCTGAGGAAAAA 60
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QY 9680 GCCAACCCGACAGACATCCCGCTCAGGTGGAATCAAGATCAAGTCAGTCGCGGC 9739
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Db 61 GCCAACCCGACAGACATCCCGCTCAGGTGGAATCAAGATCAAGTCAGTCGCGGC 120
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QY 9740 CCAGAGAACACAGGACCTCTCTTAGAGACCTTATGATACAGGCGCTCAAGATACTGA 9799
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Db 121 CCAGAGAACACAGGACCTCTCTTAGAGACCTTATGATACAGGCGCTCAAGATACTGA 180
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QY 9800 TGTGTAGTGAAGACATTTCCATTTGCGCACAGTTGACGTGAGGCAATTCGTGAATTTTC 9859
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Db 181 TGTGTAGTGAAGACATTTCCATTTGCGCACAGTTGAGGCAATTCGTGAATTTTC 240
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QY 9860 TCTCCGTCGACAGTTCCAGTATCCAGTTGTACAGTTGGCAGCTTTTGGGTGAGG 9919
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Db 241 TCTCCGTCGACAGTTCCAGTATCCAGTTGTACAGTTGTGACAGTTTGGGTGAGG 300
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QY 9920 CCGTATCCCAAGAGCAGAGATTTCCAGTATGTCAGGAGTCCCTGACCCGCACTC 9979
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Db 301 CCGTATCCCAAGAGCAGAGATTTCCAGTATGTCAGGAGTCCCTGACCCGCACTC 360
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QY 9980 ACTGCATCAACAAGCGGAACCAAGAGTGGCTTTTGTGAATTTGCAAGTGGCC 10039
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Db 361 ACTGCATCAACAAGCGGAACCAAGAGTGGCTTTTGTGAATTTGCAAGTGGCC 420
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QY 10040 CAGAGGGGCTGCACCACTACT 10060
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Db 421 CAGAGGGGCTGCACCACTACT 441
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RESULT 10
CHKPOLLI/c 2232 bp DNA linear VRT 15-OCT-1993
LOCUS
DEFINITION Gallus gallus reverse transcriptase gene, 3' end.
ACCESSION L22152
VERSION L22152.1 GI:347226
KEYWORDS POL-1 like gene.
SOURCE Gallus gallus (strain White Leghorn, sub-species domesticus) DNA.
ORGANISM Gallus gallus

MSRDPGLANGCVRTLNFGRNFKLNGSLAMIPWNAVYIKDKVOEESWLFKDA
QEVSIPLNRKVGSRDPAWLGKDLGLTRKPKGAYKLMQGRVTEEDVARDVA
RIRKAAOVLELARDYKNNKTKTFYRIGOKROTGTSPSIVNKGELTDEEFL

Db	535	ATGATGGAGCCAGGATACCACTTTGCTTTCGAGCTGCA	496
RESULT 13			
CHRPOLIC/c			
LOCUS	CHRPOLIC	1651 bp	DNA
DEFINITION	Gallus gallus POL-like gene, 3' end.		
ACCESSION	L22148		
VERSION	L22148.1	GI:347218	
KEYWORDS	POL-like gene.		
SOURCE	Gallus gallus (strain White Leghorn, sub-species domesticus) DNA.		
ORGANISM	Gallus gallus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.		
REFERENCE	1 (bases 1 to 1651)		
AUTHORS	Burch,J.B., Davis,D.L. and Haas,N.B.		
TITLE	Chicken repeat 1 elements contain a pol-like open reading frame and belong to the non-long terminal repeat class of retrotransposons		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 90 (17), 8199-8203 (1993)		
MEDLINE	93376771		
PUBMED	8396264		
FEATURES			
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	/codon_start=1		
	/label=ORF		
	/protein_id="AAA49023.1"		
	/db_xref="GI:347219"		
	/translation="LCSTKPPGGGOGKSPPTVAAEVRDLRLIDEVKSSGPDGVHP RVLEKLEVVAEPLSTIEFKSMLSIEGVPDDMRKQVYPIPKKSKEDPGNRPVLSLTS VPKRIMOILIDMLDLMRNRVY"		
BASE COUNT	405 a 360 c 531 g 355 t		
ORIGIN			
Query Match	3.2%; Score 377.6; DB 5; Length 1651;		
Best Local Similarity	79.4%; Pred. No. 3.4e-78;		
Matches 508; Conservative	0; Mismatches 104; Indels 28; Gaps 4;		
OY 10574	ATGACATATGATGATGCGCTGGGTGGAAGGACCCCAAGATCATGATCCACACC	10633	
Db 1651	ACAGATACACAGAAATGACTGGGTGGATGGACTCAAGGATCATGATCCACACCCT	1592	
OY 10634	CCCCGACAGGAGGAGCCACCAACCTCCAGATCTGTACTAGACGAGGAGCGGCT	10693	
Db 1591	ACTGC--CGTGAGAGGGCCACCAACCTCCCAT--TTACTAGACGAGGTGCCAGGCGC	1537	
OY 10694	CCATCCAACTGGCCCATGAGACACCTCCAGAGGATGAGGACCTCTCTGGGACG	10753	
Db 1536	TCATCCAACTGGGCTTGAAACACCTCCAGGAGTGGGCGATCCACAACTCTCTGGGACG	1477	
OY 10754	CTGTGCGAGCACTACCAACCTCTCTGTGAAGACTTTTCCCTACATCCAACTAAGC	10813	
Db 1476	CCATTCACAGCACTACCACTCTCTGTGAAGACTTTTCCCTACATCCAACTAAGT	1417	
OY 10814	CTTCCCTCTGAGGTGATGATCCATCTCCCTCTGTGATCATCACTGTACTCTTAAAA	10873	
Db 1416	CTTCCCTCTTTCACCTTAAACCGTTCCGCTGTGCTGTGTATCTACCTTTCAAG	1357	
OY 10874	AGTTGATTCCTCTCTTT-----TGAAGGTTGCAATGAGGTCT	10913	
Db 1356	AGTTGATTCCTCTCTTTATATAGCTCCCTTAGATCACTGAAGGCGCCAACTGAGGTCA	1297	
OY 10914	CTTTCAGACCTTCTCTCTTCGAGGATGAACAGACGACGCTCCCTGAGCTGCTTAA	10973	
Db 1296	CCCTGACG---CTTCTCTTCTCCAGGCTGAATGAAGCCCAACTCCCTTAGCTGCTCG	1240	
OY 10974	TAGGAGAGGTGCTCCAGGCTCTGATCATCTTTGTGGCCCTCTCTGGAACCGGCTCAAG	11033	

Dn	1239	CAGGGAGAGTCTCCACGCCCTGATCTCTTTTGCGCCTCTCTGTGAACCTCTTCAGC	1180
QY	11034	AGCTCACACTTTCCTGTAAGTGGGGCCCCAGGCGCTGAATCACTACAGATGGGGC	11093
Dn	1179	AGCTCTCATCTTCTTCTTACTGAGAGCTGCATCACTGACAGACAGTACCAGATGGGGC	1120
QY	11094	CTCAAAAGAGGAGTAAGAAGGGGACATCACTTCCTCACCCTGCGGCCAGCGCTCTT	11153
Dn	1119	CTCACAGAGAGATGAGTAGGAGGAGGACATCACTTCCTGCTCGCTGGGCCACTCTCTC	1060
QY	11154	CTGATGAGAGCCCTGGATACAACCTGGCTTTCGAGCTGCAA	11193
Dn	1059	ATGATGAGAGCCAGATACATTCTTTCGAGCTGCAA	1020
RESULT 14			
LOCUS	CHICKRIA/C		
DEFINITION	Gallus gallus vitellogenin gene, intron 2 with a CRI retroposon insertion.	971 bp	DNA linear VRT 03-JAN-1995
ACCESSION	M28069		
VERSION	M28069.1 GI:341819		
KEYWORDS	retroposon; vitellogenin.		
SOURCE	Gallus gallus DNA.		
ORGANISM	Gallus gallus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus; Phasianinae; Gallus.		
AUTHORS	I (bases 1 to 971)		
TITLE	Silva,R. and Burch,J.B.		
JOURNAL	Evidence that chicken CRI elements represent a novel family of retroposons		
MEDLINE	Mol. Cell. Biol. 9 (8), 3563-3566 (1989)		
PUBMED	90014816		
FEATURES	2477689		
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repeat_region	/rpt_family="CRI"		
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ORIGIN			
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Best Local Similarity	77.9% Pred. No. 1.2e-77 Indels 28 Gaps 4;		
Matches 514 Conservative 0 Mismatches 118 Indels 28 Gaps 4;			
Y 10554 AAAACCTACTTTATACATCATAGATCATAGATGAGGCTGGGTGGAGAGGACCCCAAG 10613			


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Db 966 AAAAATAATGACAGAAATGACAGAAATGACAGAAATGAGCTGGGTGGAAGGAGCCTCGAG 907

Oy 10614 GATCATGAAGATCCAAACACCCCGCCACAGAGGGGCCAACCAACCTCCAGATCTGCTACT 10673
Db 906 GATTCAGATCTCTCAACCCCTGCG--TGGGCAAGGGCCACCAACATCCCAT--TTACT 852

Oy 10674 AGACGAGCAGCCAGGCGCTCCATCCAACTGGCCATGACACCTCCAGAGGATGAGCAT 10733
Db 851 AGACGAGGTTGGCCAGGGGCCCATCCAACTGGCTTGACACCTCCAGAGGATGAGCAT 792

Oy 10734 CCACAACTCTCTGGGCAAGCTGTGCGCACACCTCCAGACCTCCAGAGGATGAGCAT 10793
Db 791 CCACAACTCTCTGGGCAAGCTGTGCGCACACCTCCAGACCTCCAGAGGATGAGCAT 732

Oy 10794 CCCTGACATCCAAATGAGCTCCCTGAGTTAGATGATGATGATGATGATGATGATGAT 10853
Db 731 CCCTGACATCCAAATGAGCTCCCTGAGTTAGATGATGATGATGATGATGATGATGAT 672

Oy 10854 CACTGTCTACTCTGTGTAAGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 10893
Db 671 TGTATCTACCTCTTCAAGAGTTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 612

Oy 10894 GGAAGGTTCATGAGTCTCTCTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 10933
Db 611 GAAAGGTTCATGAGTCTCTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 555

Oy 10954 GCTCCCTGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 11013
Db 554 GCTCCCTGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 495

Oy 11014 TCCTTGACACCGCTCTCAAGAGCTCTCAATCTCTCTCTCTCTCTCTCTCTCTCTCT 11073
Db 494 TCCTTGACACCGCTCTCAAGAGCTCTCAATCTCTCTCTCTCTCTCTCTCTCTCTCT 435

Oy 11074 TGCAGTACTCCAGATGAGGCGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 11133
Db 434 CACAGTACTCCAGATGAGGCGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 375

Oy 11134 CCCTGCTGAGCGCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 11193
Db 374 CCCTGCTGAGCGCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 315

RESULT 15
GGVITCR1/c 3297 bp DNA linear VRT 29-NOV-1987
LOCUS Chicken vitellogenin gene 3' flanking region.
DEFINITION Y00324
ACCESSION Y00324.1 GI:63883
KEYWORDS CRI repetitive sequence; vitellogenin.
SOURCE chicken.
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 3297)
REFERENCE
AUTHORS van het Schip,F., Samallo,J., Meijlink,F., Gruber,M. and AB,G.
TITLE A new repetitive element of the CRI family downstream of the
chicken vitellogenin gene
JOURNALS Nucleic Acids Res. 15 (10), 4193-4202 (1987)
MEDLINE 87230999
PUBMED 3035488
FEATURES
source 1..3297
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/note="resembling avian retroviral long terminal repeat"

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BASE COUNT 738 a 809 c 981 g 769 t
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Best Local Similarity 77.9%; Pred. No. 1.3e-77;
Matches 514; Conservative 0; Mismatches 118; Indels 28; Gaps 4;

Oy 10554 AAAACCTACTTATATCAATCATAGATATAGATGAGGCTGGGTGGAAGGAGCCCAAG 10613
Db 2691 AAAAATAATGACAGAAATGACAGAAATGACAGAAATGAGCTGGGTGGAAGGAGCCTCGAG 2632

Oy 10614 GATCATGAAGATCCAAACACCCCGCCACAGAGGGGCCAACCAACCTCCAGATCTGCTACT 10673
Db 2631 GATTCAGATCTCTCAACCCCTGCG--TGGGCAAGGGCCACCAACATCCCAT--TTACT 2577

Oy 10674 AGACGAGCAGCCAGGCGCTCCATCCAACTGGCCATGACACCTCCAGAGGATGAGCAT 10733
Db 2576 AGACGAGGTTGGCCAGGGGCCCATCCAACTGGCTTGACACCTCCAGAGGATGAGCAT 2517

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Db 2516 CCACAACTCTCTGGGCAAGCTGTGCGCACACCTCCAGACCTCCAGAGGATGAGCAT 2457

Oy 10794 CCCTGACATCCAAATGAGCTCCCTGAGTTAGATGATGATGATGATGATGATGATGAT 10853
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Oy 10894 GGAAGGTTCATGAGTCTCTCTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 10933
Db 2336 GAAAGGTTCATGAGTCTCTGACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2280

Oy 10954 GCTCCCTGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 11013
Db 2279 GCTCCCTGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2220

Oy 11014 TCCTTGACACCGCTCTCAAGAGCTCTCAATCTCTCTCTCTCTCTCTCTCTCTCTCT 11073
Db 2219 TCCTTGACACCGCTCTCAAGAGCTCTCAATCTCTCTCTCTCTCTCTCTCTCTCTCT 2160

Oy 11074 TGCAGTACTCCAGATGAGGCGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 11133
Db 2159 CACAGTACTCCAGATGAGGCGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2100

Oy 11134 CCCTGCTGAGCGCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 11193
Db 2099 CCCTGCTGAGCGCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2040

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